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OM protein - protein search, using sw model

Run on: April 12, 2005, 15:05:22 ; Search time 31.7966 seconds  
(without alignments)  
579,883 Million cell updates/sec

Title: US-09-905-247A-8

Perfect score: 1221  
Sequence: 1 DVSFRLSGATSSSYGVFISN.....VDAGVTSNALLLNPNMA 247

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A COMB pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB pep:\*  
3: /cgn2\_6/prodata/1/iaa/5A COMB pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB pep:\*  
5: /cgn2\_6/prodata/1/iaa/6B COMB pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1221	100.0	267	1	US-08-378-761A-74 Sequence 74, Appl
2	1221	100.0	267	1	US-08-485-286-74 Sequence 74, Appl
3	1212	99.3	289	1	US-07-923-692C-4 Sequence 4, Appl
4	1212	99.3	289	1	US-08-184-837-4 Sequence 4, Appl
5	1212	99.3	289	2	US-08-482-920-4 Sequence 4, Appl
6	1212	99.3	289	3	US-08-484-341-4 Sequence 4, Appl
7	1212	99.3	289	3	US-08-483-502-4 Sequence 4, Appl
8	1212	99.3	289	4	US-09-726-651A-4 Sequence 4, Appl
9	1209	99.0	247	1	US-08-488-113B-6 Sequence 6, Appl
10	1209	99.0	247	1	US-08-477-484B-6 Sequence 6, Appl
11	1209	99.0	247	2	US-08-646-360-6 Sequence 6, Appl
12	1209	99.0	247	3	US-08-839-765-6 Sequence 6, Appl
13	1209	99.0	247	3	US-09-136-389-6 Sequence 6, Appl
14	1209	99.0	247	3	US-09-610-838-6 Sequence 6, Appl
15	1209	99.0	247	4	US-09-711-485-6 Sequence 6, Appl
16	1137	93.1	255	1	US-07-901-707-6 Sequence 6, Appl
17	1137	93.1	255	1	US-07-988-430-6 Sequence 6, Appl
18	1137	93.1	255	1	US-08-425-336-6 Sequence 6, Appl
19	1137	93.1	255	5	PCT-US92-09487-6 Sequence 6, Appl
20	1071	87.7	248	3	US-08-902-486-7 Sequence 7, Appl
21	1071	87.7	290	1	US-08-245-754A-2 Sequence 2, Appl
22	1071	87.7	290	2	US-08-557-731-2 Sequence 2, Appl
23	1071	87.7	496	3	US-08-902-486-15 Sequence 15, Appl
24	802	65.7	263	1	US-07-901-707-7 Sequence 7, Appl
25	802	65.7	263	1	US-07-988-430-7 Sequence 7, Appl
26	802	65.7	263	1	US-08-425-336-7 Sequence 7, Appl
27	802	65.7	263	1	US-08-488-113B-7 Sequence 7, Appl

28	802	65.7	263	1	US-08-477-484B-7 Sequence 7, Appl
29	802	65.7	263	2	US-08-646-360-7 Sequence 7, Appl
30	802	65.7	263	3	US-08-839-765-7 Sequence 7, Appl
31	802	65.7	263	3	US-09-136-389-7 Sequence 7, Appl
32	802	65.7	263	3	US-09-610-838-7 Sequence 7, Appl
33	802	65.7	263	4	US-09-711-485-7 Sequence 7, Appl
34	802	65.7	263	5	PCT-US92-09487-7 Sequence 7, Appl
35	762	62.4	250	1	US-08-378-761A-78 Sequence 78, Appl
36	762	62.4	250	1	US-08-485-286-78 Sequence 78, Appl
37	724.5	59.3	248	1	US-07-901-707-5 Sequence 5, Appl
38	724.5	59.3	248	1	US-07-988-430-5 Sequence 5, Appl
39	724.5	59.3	248	1	US-08-425-336-5 Sequence 5, Appl
40	724.5	59.3	248	1	US-08-378-761A-75 Sequence 75, Appl
41	724.5	59.3	248	1	US-08-485-286-75 Sequence 75, Appl
42	724.5	59.3	248	1	US-08-488-113B-5 Sequence 5, Appl
43	724.5	59.3	248	1	US-08-477-484B-5 Sequence 5, Appl
44	724.5	59.3	248	2	US-08-646-360-5 Sequence 5, Appl
45	724.5	59.3	248	3	US-08-839-765-5 Sequence 5, Appl

#### ALIGNMENTS

RESULT 1  
US-08-378-761A-74  
Sequence 74, Application US/08378761A  
Patent No. 5635384  
GENERAL INFORMATION:  
APPLICANT: WALSH, TERENCE A  
APPLICANT: HEY, TIMOTHY D  
APPLICANT: MORGAN, ALICE ER  
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSER: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,761A  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 382728  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-378-761A-74  
Query Match 100.0%; Score 1221; DB 1; Length 267;  
Best Local Similarity 100.0%; Pred. No. 2.6e-119; Indels 0; Gaps 0;  
Matches 247; Conservative 0; Mismatches 0;  
1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLRSSLPQSQRYALIHITNVADETI 60  
2 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLRSSLPQSQRYALIHITNVADETI 61

QY 61 SVAIDVTNYIMGYRAGDTSYFNEASATEAAKYFKDAMRKVTLPSYGNVERLQTAAGK 120  
| | | | |  
Db 62 SVAIDVTNYIMGYRAGDTSYFNEASATEAAKYFKDAMRKVTLPSYGNVERLQTAAGK 121  
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QY 121 IRENIPGLPALDSATITLFPYNNASASALMWLIQSTSEARRYFIEQIGKRVDTKFL 180  
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Db 122 IRENIPGLPALDSATITLFPYNNASASALMWLIQSTSEARRYFIEQIGKRVDTKFL 181  
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QY 181 PSLAIIISLNSWSALSQIOIASTNNGOFESPVLINQNRVTITNVDAGVTSNIALL 240  
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Db 182 PSLAIIISLNSWSALSQIOIASTNNGOFESPVLINQNRVTITNVDAGVTSNIALL 241  
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QY 241 LNRNNMA 247  
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Db 242 LNRNNMA 248  
| | | | |

RESULT 2  
US-08-485-286-74  
; Sequence 74, Application US/08485286  
; Patent No. 5646026  
; Patent No. 5646026 5646119  
; GENERAL INFORMATION:  
; APPLICANT: WALSH, TERENCE A  
; APPLICANT: HEY, TIMOTHY D  
; APPLICANT: MORGAN, ALICE ER  
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
; TITLE OF INVENTION: USING  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: ANDREA T. BORUCKI  
; STREET: 9330 ZIONSVILLE ROAD  
; CITY: INDIANAPOLIS  
; STATE: IN  
; COUNTRY: US  
; ZIP: 46268  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,286  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/378761  
; FILING DATE: 26-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BORUCKI, ANDREA T  
; REGISTRATION NUMBER: 33651  
; REFERENCE/DOCKET NUMBER: 38272B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 337-4846  
; INFORMATION FOR SEQ ID NO: 74:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-485-286-74

Query Match 100.0%; Score 1221, DB 1, Length 267;  
Best Local Similarity 100.0%; Pred. No. 2, 6e-119,  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPSSQRYALIHLTNVADETI 60  
| | | | |  
Db 2 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPSSQRYALIHLTNVADETI 61  
| | | | |

QY 61 SVAIDVTNYIMGYRAGDTSYFNEASATEAAKYFKDAMRKVTLPSYGNVERLQTAAGK 120  
| | | | |  
Db 62 SVAIDVTNYIMGYRAGDTSYFNEASATEAAKYFKDAMRKVTLPSYGNVERLQTAAGK 121  
| | | | |  
QY 121 IRENIPGLPALDSATITLFPYNNASASALMWLIQSTSEARRYFIEQIGKRVDTKFL 180  
| | | | |  
Db 122 IRENIPGLPALDSATITLFPYNNASASALMWLIQSTSEARRYFIEQIGKRVDTKFL 181  
| | | | |  
QY 181 PSLAIIISLNSWSALSQIOIASTNNGOFESPVLINQNRVTITNVDAGVTSNIALL 240  
| | | | |  
Db 182 PSLAIIISLNSWSALSQIOIASTNNGOFESPVLINQNRVTITNVDAGVTSNIALL 241  
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QY 241 LNRNNMA 247  
| | | | |  
Db 242 LNRNNMA 248  
| | | | |

RESULT 3  
US-07-923-692C-4  
; Sequence 4, Application US/07923692C  
; Patent No. 5316931  
; GENERAL INFORMATION:  
; APPLICANT: Donson, Jon  
; APPLICANT: Dawson, William O.  
; APPLICANT: Grantcham, George L.  
; APPLICANT: Turpen, Thomas H.  
; APPLICANT: Turpen, Ann Myers  
; APPLICANT: Garger, Stephen J.  
; APPLICANT: Grillo, Laurence K.  
; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Limbach & Limbach  
; STREET: 2001 Perry Building  
; CITY: San Francisco  
; STATE: CAL  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/923,692C  
; FILING DATE: 31-JUL-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 600,244  
; FILING DATE: 22-OCT-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 641,617  
; FILING DATE: 16-JAN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 310,881  
; FILING DATE: 17-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 160,766  
; FILING DATE: 26-FEB-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 160,771  
; FILING DATE: 26-FEB-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 347,637  
; FILING DATE: 05-MAY-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 363,138  
; FILING DATE: 08-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 219,279  
; FILING DATE: 15-JUL-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: BIOG-20121  
REFERENCE/DOCKET NUMBER: USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-433-4150  
TELEFAX: 415-433-8716  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-923-692C-4

Query Match 99.3%; Score 1212; DB 1; Length 289;  
Best Local Similarity 99.2%; Pred. No. 2.5e-118;  
Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRRKALPNERKLYDIPILRRSLPGSORYALHITNVADETI 60  
DB 24 DVSFRLSGATSSSYGVFISNLRRKALPNERKLYDIPILRRSLPGSORYALHITNVADETI 83  
QY 61 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVFKDMARKVTLPSGNYERLQTPAAGK 120  
DB 84 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVFKDMARKVTLPSGNYERLQTPAAGK 143  
QY 121 IRENIPGLGPAIDSAITTLFFYNNANSASALMWLIQSTSEARXYKIEQOIGKRVDKTFL 180  
DB 144 IRENIPGLGPAIDSAITTLFFYNNANSASALMWLIQSTSEARXYKIEQOIGKRVDKTFL 203  
QY 181 PSIAIISLENSWSALSKQIQIASTNNQGFESPVVLIINAQORVTITNVDAVVTSNIALL 240  
DB 204 PSIAIISLENSWSALSKQIQIASTNNQGFETPVVLIINAQORVTITNVDAVVTSNIALL 263  
QY 241 LNRNNMA 247  
DB 264 LNRNNMA 270

RESULT 4  
US-08-184-237-4  
Sequence 4, Application US/08184237  
Patent No. 5589367  
GENERAL INFORMATION:  
APPLICANT: Donson, Jon  
APPLICANT: Dawson, William O.  
APPLICANT: Grantham, George L.  
APPLICANT: Turpen, Thomas H.  
APPLICANT: Turpen, Ann Myers  
APPLICANT: Garger, Stephen J.  
APPLICANT: Grill, Laurence K.  
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Limbach & Limbach  
STREET: 2001 Ferry Building  
CITY: San Francisco  
STATE: CAL  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/184,237  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 923,692  
FILING DATE: 31-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 600,244  
FILING DATE: 22-OCT-1990

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 641,617  
FILING DATE: 16-JAN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 310,881  
FILING DATE: 17-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 160,766  
FILING DATE: 26-FEB-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 160,771  
FILING DATE: 26-FEB-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 347,637  
FILING DATE: 05-MAY-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 363,138  
FILING DATE: 08-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 219,279  
FILING DATE: 15-JUL-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: BIOG-20121 USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-433-4150  
TELEFAX: 415-433-8716  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-184-237-4

Query Match 99.3%; Score 1212; DB 1; Length 289;  
Best Local Similarity 99.2%; Pred. No. 2.5e-118;  
Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRRKALPNERKLYDIPILRRSLPGSORYALHITNVADETI 60  
DB 24 DVSFRLSGATSSSYGVFISNLRRKALPNERKLYDIPILRRSLPGSORYALHITNVADETI 83  
QY 61 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVFKDMARKVTLPSGNYERLQTPAAGK 120  
DB 84 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVFKDMARKVTLPSGNYERLQTPAAGK 143  
QY 121 IRENIPGLGPAIDSAITTLFFYNNANSASALMWLIQSTSEARXYKIEQOIGKRVDKTFL 180  
DB 144 IRENIPGLGPAIDSAITTLFFYNNANSASALMWLIQSTSEARXYKIEQOIGKRVDKTFL 203  
QY 181 PSIAIISLENSWSALSKQIQIASTNNQGFESPVVLIINAQORVTITNVDAVVTSNIALL 240  
DB 204 PSIAIISLENSWSALSKQIQIASTNNQGFETPVVLIINAQORVTITNVDAVVTSNIALL 263  
QY 241 LNRNNMA 247  
DB 264 LNRNNMA 270

RESULT 5  
US-08-482-920-4  
Sequence 4, Application US/08482920  
Patent No. 5866785  
GENERAL INFORMATION:  
APPLICANT: Donson, Jon  
APPLICANT: Dawson, William O.  
APPLICANT: Grantham, George L.  
APPLICANT: Turpen, Thomas H.  
APPLICANT: Turpen, Ann Myers  
APPLICANT: Garger, Stephen J.  
APPLICANT: Grill, Laurence K.



Query Match 99.3%; Score 1212; DB 3; Length 289;  
 Best Local Similarity 99.2%; Pred. No. 2.5e-118;  
 Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 60  
 DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 83  
 QY 61 SVAIDVTNVIYINGRAGDTSYFENEASATEAKVFKDAMRKVTLPSGNYERLQTPAGK 120  
 DB 84 SVAIDVTNVIYINGRAGDTSYFENEASATEAKVFKDAMRKVTLPSGNYERLQTPAGK 143  
 QY 121 IRENIPGLPALDSATITLTFYNNANASALMWLIQSTSEARKYFIEQOIGKRVKDTFL 180  
 DB 144 IRENIPGLPALDSATITLTFYNNANASALMWLIQSTSEARKYFIEQOIGKRVKDTFL 203  
 QY 181 PSIAIISLNSWSALSQKQIQAISTNNGQFESSPVVLIINAQORVTITNVDAGVVTSNIAL 240  
 DB 204 PSIAIISLNSWSALSQKQIQAISTNNGQFETPVVLIINAQORVMTNVDAGVVTSNIAL 263  
 QY 241 LNRNMA 247  
 DB 264 LNRNMA 270

RESULT 7  
 US-08-483-502-4  
 ; Sequence 4, Application US/08483502  
 ; Patent No. 6284492  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donson, Jon  
 ; APPLICANT: Dawson, William O.  
 ; APPLICANT: Grantham, George L.  
 ; APPLICANT: Turpen, Thomas H.  
 ; APPLICANT: Turpen, Ann M.  
 ; APPLICANT: Garger, Stephen J.  
 ; APPLICANT: Grill, Laurence K.  
 ; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 ; STREET: 1201 New York Avenue N.W., Suite 1000  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/483,502  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/739,143  
 ; FILING DATE:  
 ; APPLICATION NUMBER: US 600,244  
 ; FILING DATE: 22-OCT-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 641,617  
 ; FILING DATE: 16-JAN-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 310,881  
 ; FILING DATE: 17-FEB-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 160,766  
 ; FILING DATE: 26-FEB-1988  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 160,771  
 ; FILING DATE: 26-FEB-1988  
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 347,637  
 FILING DATE: 05-MAY-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 363,138  
 FILING DATE: 08-JUN-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 219,279  
 FILING DATE: 15-JUL-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 18604-090574  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEFAX: 202-962-8300  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 289 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-483-502-4

Query Match 99.3%; Score 1212; DB 3; Length 289;  
 Best Local Similarity 99.2%; Pred. No. 2.5e-118;  
 Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 60  
 DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 83  
 QY 61 SVAIDVTNVIYINGRAGDTSYFENEASATEAKVFKDAMRKVTLPSGNYERLQTPAGK 120  
 DB 84 SVAIDVTNVIYINGRAGDTSYFENEASATEAKVFKDAMRKVTLPSGNYERLQTPAGK 143  
 QY 121 IRENIPGLPALDSATITLTFYNNANASALMWLIQSTSEARKYFIEQOIGKRVKDTFL 180  
 DB 144 IRENIPGLPALDSATITLTFYNNANASALMWLIQSTSEARKYFIEQOIGKRVKDTFL 203  
 QY 181 PSIAIISLNSWSALSQKQIQAISTNNGQFESSPVVLIINAQORVTITNVDAGVVTSNIAL 240  
 DB 204 PSIAIISLNSWSALSQKQIQAISTNNGQFETPVVLIINAQORVMTNVDAGVVTSNIAL 263  
 QY 241 LNRNMA 247  
 DB 264 LNRNMA 270

RESULT 8  
 US-09-726-651A-4  
 ; Sequence 4, Application US/09726651A  
 ; Patent No. 6448046  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donson, Jon  
 ; APPLICANT: Dawson, William O.  
 ; APPLICANT: Grantham, George L.  
 ; APPLICANT: Turpen, Thomas H.  
 ; APPLICANT: Turpen, Ann M.  
 ; APPLICANT: Garger, Stephen J.  
 ; APPLICANT: Grill, Laurence K.  
 ; TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS  
 ; FILE REFERENCE: 008010023CNU501  
 ; CURRENT APPLICATION NUMBER: US/09/726,651A  
 ; CURRENT FILING DATE: 2002-05-02  
 ; PRIOR APPLICATION NUMBER: 08/483,502  
 ; PRIOR FILING DATE: 1995-06-07  
 ; PRIOR APPLICATION NUMBER: 08/184,237  
 ; PRIOR FILING DATE: 1994-01-19  
 ; PRIOR APPLICATION NUMBER: 07/923,692  
 ; PRIOR FILING DATE: 1992-07-31  
 ; PRIOR APPLICATION NUMBER: 07/600,244  
 ; PRIOR FILING DATE: 1990-10-22  
 ; PRIOR APPLICATION NUMBER: 07/641,617

;; PRIOR FILING DATE: 1991-01-16  
;; PRIOR APPLICATION NUMBER: 07/737,899  
;; PRIOR FILING DATE: 1991-07-26  
;; NUMBER OF SEQ ID NOS: 19  
;; SOFTWARE: FaastSeq for Windows Version 4.0  
;; SEQ ID NO: 4  
;; LENGTH: 289  
;; TYPE: PRT  
;; ORGANISM: Chinese cucumber alpha-trichosanthin  
US-09-726-651A-4

Query Match 99.3%; Score 1212; DB 4; Length 289;  
Best Local Similarity 99.2%; Pred. No. 2,5e-118;  
Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORYALHILNTYADETI 60  
DB 24 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORYALHILNTYADETI 83  
QY 61 SVAIDVTNYIMGYRAGDTSYFPNEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120  
DB 84 SVAIDVTNYIMGYRAGDTSYFPNEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 143  
QY 121 IRENIPGLPALDSATITLFFYNNANSAASALMWLIQSTSEARARYFIEQIGKRVDKTFL 180  
DB 144 IRENIPGLPALDSATITLFFYNNANSAASALMWLIQSTSEARARYFIEQIGKRVDKTFL 203  
QY 181 PSIAIISLNSWSALSKQIQIASTNNGQFESPVVLIINAQORVTITNVDAVVTSNIALL 240  
DB 204 PSIAIISLNSWSALSKQIQIASTNNGQFESPVVLIINAQORVTITNVDAVVTSNIALL 263  
QY 241 LNRNNMA 247  
DB 264 LNRNNMA 270

## RESULT 9

US-08-488-113B-6  
; Sequence 6, Application US/08488113B  
; Patent No. 5744580  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,113B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/901,707  
;; FILING DATE: 19-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/787,567  
;; FILING DATE: 04-NOV-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: McNicholas, Janet M.  
;; REGISTRATION NUMBER: 32,918  
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 312/707-8889  
;; TELEFAX: 312/707-9155  
;; TELEX: 650 388-1248  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 247 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULAR TYPE: protein  
US-08-488-113B-6

Query Match 99.0%; Score 1209; DB 1; Length 247;  
Best Local Similarity 99.2%; Pred. No. 4.1e-118;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORYALHILNTYADETI 60  
DB 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORYALHILNTYADETI 60  
QY 61 SVAIDVTNYIMGYRAGDTSYFPNEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120  
DB 61 SVAIDVTNYIMGYRAGDTSYFPNEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120  
QY 121 IRENIPGLPALDSATITLFFYNNANSAASALMWLIQSTSEARARYFIEQIGKRVDKTFL 180  
DB 121 IRENIPGLPALDSATITLFFYNNANSAASALMWLIQSTSEARARYFIEQIGKRVDKTFL 180  
QY 181 PSIAIISLNSWSALSKQIQIASTNNGQFESPVVLIINAQORVTITNVDAVVTSNIALL 240  
DB 181 PSIAIISLNSWSALSKQIQIASTNNGQFESPVVLIINAQORVTITNVDAVVTSNIALL 240  
QY 241 LNRNNMA 247  
DB 241 LNRNNMA 247

## RESULT 10

US-08-477-484B-6  
; Sequence 6, Application US/08477484B  
; Patent No. 5756699  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,484B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-484B-6

Query Match 99.0%; Score 1209; DB 1; Length 247;  
Best Local Similarity 99.2%; Pred. No. 4.1e-118;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSORYALHILTNVADETI 60  
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSORYALHILTNVADETI 60  
QY 61 SVAIDVTNNYIMGYRAGDTSYFPNEASATEAAKYVFKDMARKYTLTPYSGYERLQTPAGK 120  
DB 61 SVAIDVTNNYIMGYRAGDTSYFPNEASATEAAKYVFKDMARKYTLTPYSGYERLQTPAGK 120  
QY 121 IRENIPGLPALDSATTLTFYNNANSAALMWLLOSTSEAAKYKIEQOIGRVKXFL 180  
DB 121 IRENIPGLPALDSATTLTFYNNANSAALMWLLOSTSEAAKYKIEQOIGRVKXFL 180  
QY 181 PSIAIISLENSWSALSKQIOIASSTNGQFESPVLINAQORVLTITNVDAVGTSTNIAL 240  
DB 181 PSIAIISLENSWSALSKQIOIASSTNGQFESPVLINAQORVLTITNVDAVGTSTNIAL 240  
QY 241 LNNNNMA 247  
DB 241 LNNNNMA 247  
RESULT 11  
US-08-646-360-6  
Sequence 6, Application US/08646360  
Patent No. 5837491  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studinka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA

ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-360-6

Query Match 99.0%; Score 1209; DB 2; Length 247;  
Best Local Similarity 99.2%; Pred. No. 4.1e-118;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSORYALHILTNVADETI 60  
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSORYALHILTNVADETI 60  
QY 61 SVAIDVTNNYIMGYRAGDTSYFPNEASATEAAKYVFKDMARKYTLTPYSGYERLQTPAGK 120  
DB 61 SVAIDVTNNYIMGYRAGDTSYFPNEASATEAAKYVFKDMARKYTLTPYSGYERLQTPAGK 120  
QY 121 IRENIPGLPALDSATTLTFYNNANSAALMWLLOSTSEAAKYKIEQOIGRVKXFL 180  
DB 121 IRENIPGLPALDSATTLTFYNNANSAALMWLLOSTSEAAKYKIEQOIGRVKXFL 180  
QY 181 PSIAIISLENSWSALSKQIOIASSTNGQFESPVLINAQORVLTITNVDAVGTSTNIAL 240  
DB 181 PSIAIISLENSWSALSKQIOIASSTNGQFESPVLINAQORVLTITNVDAVGTSTNIAL 240  
QY 241 LNNNNMA 247  
DB 241 LNNNNMA 247  
RESULT 12  
US-08-839-765-6  
Sequence 6, Application US/08839765  
Patent No. 614631  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSER: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/839,765  
FILING DATE: 15-APR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-839-765-6

Query Match 99.0%; Score 1209; DB 3; Length 247;  
Best Local Similarity 99.2%; Pred. No. 4.1e-118;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60  
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60  
QY 61 SVVADVTNVIYIMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPSYGNVERLQTAAGK 120  
DB 61 SVVADVTNVIYIMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPSYGNVERLQTAAGK 120  
QY 121 IRENIPLGIPALDSATITLFFYNNANSAASALMWLLOSTSEAAKYRTEEOIGRVYKTF 180  
DB 121 IRENIPLGIPALDSATITLFFYNNANSAASALMWLLOSTSEAAKYRTEEOIGRVYKTF 180  
QY 181 PSLAIIISLNSWSALSKOIOIASTNNGOESPVLINAOQRVTITNVAGVYTSNIAL 240  
DB 181 PSLAIIISLNSWSALSKOIOIASTNNGOESPVLINAOQRVTITNVAGVYTSNIAL 240  
QY 241 IIRNNMA 247  
|||||

DB 241 IIRNNMA 247

RESULT 13  
US-09-136-389-6  
Sequence 6, Application US/09136389  
Patent No. 6146850  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSER: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-136-389-6

Query Match 99.0%; Score 1209; DB 3; Length 247;  
Best Local Similarity 99.2%; Pred. No. 4.1e-118;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60  
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60  
QY 61 SVVADVTNVIYIMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPSYGNVERLQTAAGK 120  
|||||



Db 61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKDMARKVTLPYSGNYERLQTPAGK 120  
QY 121 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFEQOIGKRVDTFL 180  
121 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFEQOIGKRVDTFL 180  
QY 181 PSIAITISLNSWSALSQKQIQIASTNNQGFESPVLINAOQRVTITNVDAVVTSNIAL 240  
Db 181 PSIAITISLNSWSALSQKQIQIASTNNQGFESPVLINAOQRVTITNVDAVVTSNIAL 240  
QY 241 LNRNNMA 247  
241 LNRNNMA 247  
Db 241 LNRNNMA 247

RESULT 14  
US-09-610-838-6  
; Sequence 6, Application US/09610838  
; Patent No. 6376217  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/610,838  
; FILING DATE: 06-JUL-2000  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/136,389  
; FILING DATE: 18-AUG-1998  
; APPLICATION NUMBER: 08/646,360  
; FILING DATE: 13-MAY-1996  
; APPLICATION NUMBER: PCT/US94/05348  
; FILING DATE: 12-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 200-70, P4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 amino acids  
; TYPE: amino acid

TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-610-838-6  
Query Match 99.0%; Score 1209; DB 3; Length 247;  
Best Local Similarity 99.2%; Pred. No. 4,1e-118;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DVSFRLSGATSSSGYGFISNLKRALPNERKLYDIPILRSLSPLSGQRYALIHLTNVADDTI 60  
1 DVSFRLSGATSSSGYGFISNLKRALPNERKLYDIPILRSLSPLSGQRYALIHLTNVADDTI 60  
Db 1 DVSFRLSGATSSSGYGFISNLKRALPNERKLYDIPILRSLSPLSGQRYALIHLTNVADDTI 60  
QY 61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKDMARKVTLPYSGNYERLQTPAGK 120  
Db 61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKDMARKVTLPYSGNYERLQTPAGK 120  
QY 121 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFEQOIGKRVDTFL 180  
Db 121 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFEQOIGKRVDTFL 180  
QY 181 PSIAITISLNSWSALSQKQIQIASTNNQGFESPVLINAOQRVTITNVDAVVTSNIAL 240  
Db 181 PSIAITISLNSWSALSQKQIQIASTNNQGFESPVLINAOQRVTITNVDAVVTSNIAL 240  
QY 241 LNRNNMA 247  
241 LNRNNMA 247  
Db 241 LNRNNMA 247

RESULT 15  
US-09-711-485-6  
; Sequence 6, Application US/09711485  
; Patent No. 6649742  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/711,485  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/839,765  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-711-485-6

Query Match 99.0%; Score 1209; DB 4; Length 247;  
Best local Similarity 99.2%; Pred. No. 4,1e-118;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPLLRSSLPGSQRYALIHLTNVADETI	60
Db	1	DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPLLRSSLPGSQRYALIHLTNVADETI	60
QY	61	SVADIVTNYIMGYRAGDTSYFPNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAAGK	120
Db	61	SVADIVTNYIMGYRAGDTSYFPNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAAGK	120
QY	121	IRENIPLGHPALDSAITTLFPYNNANSASALMWLIOSTSEAAKYKFIEOQIGKVDKFTL	180
Db	121	IRENIPLGHPALDSAITTLFPYNNANSASALMWLIOSTSEAAKYKFIEOQIGKVDKFTL	180
QY	181	PSLAISLSENSWALSKEQIQIASTNNGQFESPVLINAOQVATITNVDAGVVTSNIALL	240
Db	181	PSLAISLSENSWALSKEQIQIASTNNGQFESPVLINAOQVATITNVDAGVVTSNIALL	240
QY	241	LNRRNMA 247	
Db	241	LNRRNMA 247	

Search completed: April 12, 2005, 15:16:15  
Job time : 32.7966 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 12, 2005, 14:53:56 ; Search time 111.519 Seconds

(without alignments)  
856.626 Million cell updates/sec

Title: US-09-905-247A-8

Perfect score: 1221  
Sequence: 1 DVSPRLSGATSSSYGVFIN.....VDAGVTSNALLNNMMA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1221	100.0	247	3	AAV69048
2	1221	100.0	248	2	AAV69048
3	1221	100.0	248	2	AAV69048
4	1221	100.0	248	2	AAV69048
5	1221	100.0	248	2	AAV69048
6	1221	100.0	248	2	AAV69048
7	1221	100.0	248	2	AAV69048
8	1221	100.0	248	2	AAV69048
9	1221	100.0	248	2	AAV69048
10	1221	100.0	248	2	AAV69048
11	1221	100.0	248	2	AAV69048
12	1221	100.0	248	2	AAV69048
13	1221	100.0	248	2	AAV69048
14	1221	100.0	248	2	AAV69048
15	1221	100.0	248	2	AAV69048
16	1221	100.0	248	2	AAV69048
17	1221	100.0	248	2	AAV69048
18	1221	100.0	248	2	AAV69048
19	1221	100.0	248	2	AAV69048
20	1221	100.0	248	2	AAV69048
21	1221	100.0	248	2	AAV69048
22	1221	100.0	248	2	AAV69048
23	1221	100.0	248	2	AAV69048
24	1221	100.0	248	2	AAV69048
25	1221	100.0	248	2	AAV69048

26	1137	93.1	255	2	AAV37295	AAV37295 Plant typ
27	1137	93.1	255	2	AAV37295	AAV37295 Plant typ
28	1071	87.7	247	3	AAV69043	AAV69043 Amino aci
29	1071	87.7	248	4	AAV68824	AAV68824 Residues
30	1071	87.7	267	8	AAV01299	AAV01299 Wild type
31	1071	87.7	267	8	AAV05683	AAV05683 Blyonla d
32	1071	87.7	290	2	AAV92481	AAV92481 Blyonlin 1
33	1071	87.7	496	4	AAV68828	AAV68828 B11-Q28-5
34	1044	85.5	267	3	AAV01300	AAV01300 Altered b
35	886	72.6	267	8	AAV05689	AAV05689 Blyonla d
36	802	65.7	263	2	AAV63908	AAV63908 Type I ri
37	802	65.7	263	2	AAV74182	AAV74182 Type I ri
38	795	65.1	263	2	AAV37296	AAV37296 Plant typ
39	762	62.4	250	2	AAV21707	AAV21707 Memordin
40	762	62.4	250	2	AAV25144	AAV25144 Memordin
41	754	61.8	277	2	AAV29909	AAV29909 Prod. of
42	740	60.6	272	2	AAV07522	AAV07522 Alpha-Tri
43	740	60.6	272	2	AAV25577	AAV25577 Ribosome
44	728.5	59.7	278	2	AAV29910	AAV29910 Prod. of
45	728.5	59.7	280	2	AAV07521	AAV07521 Alpha-Tri

## ALIGNMENTS

RESULT 1	AAV69048	standard; protein; 247 AA.
ID	AAV69048	standard; protein; 247 AA.
AC	AAV69048	
DT	06-AUG-2003	(revised)
DT	30-MAY-2000	(first entry)
XX	Amino acid sequence of exemplary cell toxin trichosanthin.	
XX	Chemokine receptor; ligand; inflammatory response; immune effector cell;	
XX	secondary tissue damage; central nervous system injury; trichosanthin;	
XX	CNS inflammatory disease; neurodegenerative disorder; heart disease;	
XX	inflammatory eye disease; inflammatory bowel disease; PCR primer;	
XX	inflammatory joint disease; inflammatory kidney; renal disease;	
XX	inflammatory lung disease; inflammatory nasal disease; thyroiditis;	
XX	inflammatory thyroid disease; cytokine-regulated cancer; se.	
OS	Trichosanthes kirilowii.	
PN	WO200004926-A2.	
XX	03-FEB-2000.	
PD	21-JUL-1999; 99WO-CA000659.	
PF	22-JUL-1998; 98US-00120523.	
PR	(OSPR-) OSPREY PHARM LTD.	
PA	McDonald JR, Coggin PJ;	
PI	WPI; 2000-182542/16.	
PT	A new therapeutic agent comprising a conjugate for treating secondary	
PT	tissue damage and other disease conditions like Alzheimer's disease,	
PT	stroke, Parkinson's disease and atherosclerosis.	
PS	Disclosure; Page 67; 204pp; English.	
XX	The present sequence represents an exemplary cell toxin, which can be	
XX	incorporated into the conjugates of the invention. The specification	
XX	describes a conjugate, comprising a targeted agent and a chemokine	
XX	receptor ligand. The conjugate binds to a chemokine receptor resulting in	
XX	internalisation of the targeted agent in cells bearing the receptor. The	
XX	conjugates are used for formulating a medicament or for treating	
XX	disorders associated with inflammatory responses resulting from	

CC activation, proliferation and migration of immune effector cells. The  
CC disorders or disease states comprise secondary tissue damage such as  
CC central nervous system (CNS) injury, CNS inflammatory diseases,  
CC neurodegenerative disorders, heart disease, inflammatory eye diseases,  
CC inflammatory bowel diseases, inflammatory joint diseases, inflammatory  
CC kidney or renal diseases, inflammatory lung diseases, inflammatory nasal  
CC diseases, inflammatory thyroid disease such as thyroiditis, or cytokine-  
CC regulated cancers. (Updated on 06-AUG-2003 to correct OS field.)

XX SQ Sequence 247 AA;

Query Match 100.0%; Score 1221; DB 3; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9e-111;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNYADETI 60  
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNYADETI 60  
QY 61 SVAIDVTNVIYMGYAGDTSYFPNESAATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120  
DB 61 SVAIDVTNVIYMGYAGDTSYFPNESAATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120  
QY 121 IRENIPLGIPALDSAITTLFFYNANSAASALMWLIQSTSEARARYKFEIQIGKRVDTFPL 180  
DB 121 IRENIPLGIPALDSAITTLFFYNANSAASALMWLIQSTSEARARYKFEIQIGKRVDTFPL 180  
QY 181 PSLAIISLSENSWSALSQIQIASTNNQGFESPVLINQONRVITTNVDAGVTSNIALL 240  
DB 181 PSLAIISLSENSWSALSQIQIASTNNQGFESPVLINQONRVITTNVDAGVTSNIALL 240  
QY 241 LNRNNMA 247  
DB 241 LNRNNMA 247

RESULT 2  
AAR07518  
ID AAR07518 standard; protein; 248 AA.

XX AC AAR07518;

XX DT 06-FEB-1991 (first entry)

XX DE Synthetic alpha-trichosanthin.

XX KW trichosanthin (TCS); Human Immunodeficiency Virus; inhibition.

XX OS Trichosanthes kirilowii.

XX PN WO9012097-A.

XX PD 18-OCT-1990.

XX PF 04-APR-1989; 89US-00333184.

XX PR 04-APR-1989; 89US-00333184.

XX PA (GENE-) GENELABS INC.

XX PI Platek M, Chow T, Fry K;

XX DR WPI: 1990-334847/44.

XX DR N-PSDB; AAQ06346.

PT Recombinant tri:chosanthin protein - with selective inhibitory effect on  
PT viral expression in HIV infected T-cells or monocyte-macrophase.

XX PS Example; Fig 11; 102pp; English.

CC Encoded by a synthetic gene containing unique restriction sites spaced 20  
CC to 90 bp apart. Introduction of mutations is facilitated by cassette  
CC replacement. The effect of mutations on inhibitory action can be

CC investigated. For example, a double mutant containing the amino acid  
CC substitutions Glu(160) to Asp and Arg(163) to Lys was found to be almost  
CC 3 logs less active at inhibiting in vitro translation in rabbit  
CC reticulocyte lysate. See also AAQ06343-5 and AAQ06347-Q06351

XX SQ Sequence 248 AA;

Query Match 100.0%; Score 1221; DB 2; Length 248;  
Best Local Similarity 100.0%; Pred. No. 9.1e-111;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNYADETI 60  
DB 2 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNYADETI 61  
QY 61 SVAIDVTNVIYMGYAGDTSYFPNESAATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120  
DB 62 SVAIDVTNVIYMGYAGDTSYFPNESAATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 121  
QY 121 IRENIPLGIPALDSAITTLFFYNANSAASALMWLIQSTSEARARYKFEIQIGKRVDTFPL 180  
DB 122 IRENIPLGIPALDSAITTLFFYNANSAASALMWLIQSTSEARARYKFEIQIGKRVDTFPL 181  
QY 181 PSLAIISLSENSWSALSQIQIASTNNQGFESPVLINQONRVITTNVDAGVTSNIALL 240  
DB 182 PSLAIISLSENSWSALSQIQIASTNNQGFESPVLINQONRVITTNVDAGVTSNIALL 241  
QY 241 LNRNNMA 247  
DB 242 LNRNNMA 248

RESULT 3  
AAR25573  
ID AAR25573 standard; protein; 248 AA.

XX AC AAR25573;

XX DT 25-MAR-2003 (revised)

XX DT 13-JAN-1993 (first entry)

XX DE Mature alpha-Trichosanthin.

XX KW TCS; alpha-trichosanthin; Radix trichosanthin; abortifacient;  
XX ribosome inactivating protein; RIP; HIV-infected human T cells;  
XX human immunodeficiency virus; Trichosanthes kirilowii; ss.

XX OS Synthetic.

XX PN US5128460-A.

XX PD 07-JUL-1992.

XX PF 04-APR-1990; 90US-00504775.

XX PR 04-APR-1989; 89US-00333184.

XX PR 07-SEP-1989; 89US-00404326.

XX PA (GENE-) GENELABS INC.

XX PI Platek M, Chow TP, Fry K;

XX DR WPI: 1992-249485/30.

XX DR N-PSDB; AAQ25573.

PT Nucleic acid encoding trichosanthin protein - which can be used to  
PT inactivate ribosome(s) to inhibit protein synthesis or to inhibit HIV  
PT expression.

XX PS Example 6; Fig 11; 53pp; English.

CC A synthetic alpha-trichosanthin gene was constructed to facilitate  
CC mutational analysis of alpha-TCS in experiments to investigate structure-

CC function relationships. The synthetic gene contains unique restriction  
CC sites spaced 20-90bp apart. The translation product of the synthetic gene  
CC corresponds to the mature alpha-TCS. Variants of the protein can be  
CC generated by mutagenesis of the synthetic gene. The variants can then be  
CC screened for changes in ribosome inhibitory and/or HIV-1 inhibitory  
CC activities. See AAQ26499-Q26505. (Updated on 25-MAR-2003 to correct PF  
CC field.) (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 248 AA;

Query Match

Best Local Similarity 100.0%; Score 1221; DB 2; Length 248;

Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSGYGFISNLKRALPNERKLYDIPILRSLSPGSQRYALHILTNVADDTI 60

DB 2 DVSFRLSGATSSGYGFISNLKRALPNERKLYDIPILRSLSPGSQRYALHILTNVADDTI 61

QY 61 SVADVTNVIYIMGYRAGDTSYFFNEASATEAKYVFDKMRKVTLPYSGYERLQTPACK 120

DB 62 SVADVTNVIYIMGYRAGDTSYFFNEASATEAKYVFDKMRKVTLPYSGYERLQTPACK 121

QY 121 IRENIPILGLPALDSATITLTFYNNANSASALMWLIQSTSEARARYKFEQOIGKRVKXFL 180

DB 122 IRENIPILGLPALDSATITLTFYNNANSASALMWLIQSTSEARARYKFEQOIGKRVKXFL 181

QY 181 PSIAITISLENSWSALSKQIQIASTNNQGFESPVLINAQNRVTITNVDAVVTISNALL 240

DB 182 PSIAITISLENSWSALSKQIQIASTNNQGFESPVLINAQNRVTITNVDAVVTISNALL 241

QY 241 LNRRNMA 247

DB 242 LNRRNMA 248

RESULT 4

AAW21703

ID AAW21703 standard; protein; 267 AA.

XX AAW21703;

DT 25-MAR-2003 (revised)

DT 26-SEP-1997 (first entry)

XX Trichosanthin.

XX pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;

KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;

KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat;

KW ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.

XX Trichosanthes kirilowii.

XX Key Location/Qualifiers

FT Region 139..149

FT /note="Position of possible insertion of internal

peptide linker sequence"

XX US5635384-A.

PD 03-JUN-1997.

XX 26-JAN-1995; 95US-00378761.

XX 11-JUN-1990; 90US-00535636.

PR 09-DEC-1992; 92US-00987927.

XX (DOWC) DOWELANCO.

XX Hey TD, Morgan AER, Walsh TA;

XX WPI, 1997-309831/28.

PT Inactive precursor of maize ribosome-inactivating protein - also chimeric  
PT ribosome-inactivating protein precursors containing internal linker  
PT sequences.

XX Claim 2; Col 115-118; 121p; English.

CC The sequences given in AAW21698-710 represent Ribosome Inactivating  
CC Proteins (RIP's), which may be used in the construction of the proRIP of  
CC the invention. The proRIP has a selectively removable, internal peptide  
CC linker. The precursor sequence is incapable of inactivating eukaryotic  
CC ribosomes, but can be converted by removal of the linker into a protein  
CC having alpha and beta fragments and being capable of inactivating  
CC eukaryotic ribosomes. RIPs are potent inhibitors of eukaryotic protein  
CC synthesis. They possess a highly specific N-glycosidase activity which  
CC cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 28S  
CC RNA. RIPs selectively inhibit cellular proliferation of cells, e.g.  
CC cancer cells and HIV-infected T cells. The inactive proRIP proteins make  
CC it possible to provide protein synthesis inhibitors with uses in  
CC practical and improved ways not before possible. The RIP can be used to  
CC make cytotoxic conjugates. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 267 AA;

Query Match

Best Local Similarity 100.0%; Score 1221; DB 2; Length 267;

Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSGYGFISNLKRALPNERKLYDIPILRSLSPGSQRYALHILTNVADDTI 60

DB 2 DVSFRLSGATSSGYGFISNLKRALPNERKLYDIPILRSLSPGSQRYALHILTNVADDTI 61

QY 61 SVADVTNVIYIMGYRAGDTSYFFNEASATEAKYVFDKMRKVTLPYSGYERLQTPACK 120

DB 62 SVADVTNVIYIMGYRAGDTSYFFNEASATEAKYVFDKMRKVTLPYSGYERLQTPACK 121

QY 121 IRENIPILGLPALDSATITLTFYNNANSASALMWLIQSTSEARARYKFEQOIGKRVKXFL 180

DB 122 IRENIPILGLPALDSATITLTFYNNANSASALMWLIQSTSEARARYKFEQOIGKRVKXFL 181

QY 181 PSIAITISLENSWSALSKQIQIASTNNQGFESPVLINAQNRVTITNVDAVVTISNALL 240

DB 182 PSIAITISLENSWSALSKQIQIASTNNQGFESPVLINAQNRVTITNVDAVVTISNALL 241

QY 241 LNRRNMA 247

DB 242 LNRRNMA 248

RESULT 5

AAW25140

ID AAW25140 standard; protein; 267 AA.

XX AAW25140;

DT 25-MAR-2003 (revised)

DT 02-DEC-1997 (first entry)

XX Trichosanthin (a ribosome inhibitory protein) inactive precursor.

KW Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;  
KW internal linker; Barley Translation Inhibitor; Trichosanthin;  
KW Ricin A-chain; Abrin-A-chain; Saporin; SLT-1; Luffin-A; MAP;  
KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;  
KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;  
KW post-translational modification; cancer; neoplasia; HIV; AIDS;  
KW human immunodeficiency virus; acquired immune deficiency syndrome.

XX Synthetic.

XX US5646026-A.

XX 08-JUL-1997.

```

PF 07-JUN-1995; 95US-00485286.
XX
XX 11-JUN-1990; 90US-00535636.
PR 09-DEC-1992; 92US-00987927.
PR 26-JAN-1995; 95US-00378761.
XX
XX (DOMC ) DOWELANCO.
XX
XX Hey TD, Morgan AER, Walsh TA;
XX
XX WPI; 1997-362934/33.
XX
XX DNA encoding pro-ribosome inactivating proteins - inactive precursors of
XX ribosome inactivating proteins; can be expressed in eukaryotic cells
XX without causing cell death.
XX
XX Claim 4; Col 115-118; 186pp; English.
XX
XX AAW25140 shows a Trichosanthin (ribosome inhibitory protein, RIP) protein
XX which was engineered to contain a selectively removable internal peptide
XX linker sequence separating the alpha and beta units of the RIP. When
XX separated the two units regain activity and are capable of inactivating
XX eukaryotic ribosomes and hence preventing protein production. Many
XX different RIPs may be produced with an internal linker including maize
XX RIP, Trichosanthin, Ricin A-chain, Abrin A-chain and Saportin. The Ribs
XX can be used in the construction of therapeutic toxins targeted to
XX specific cells such as tumour cells via the attachment of a targeting
XX polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy
XX (see US4869903). There is interest in expressing RIP recombinantly in
XX host eukaryotic cells, because of the capacity to provide correct post-
XX translational processing. However, Ribs effectively inhibit protein
XX synthesis in eukaryotic cells resulting in cell death. Since the inactive
XX RIP proteins are not cytotoxic to eukaryotic cells, they can be
XX recombinantly expressed in such cells and then converted to active RIP
XX proteins. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 267 AA;
SQ
Query Match 100.0%; Score 1221; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSGRYALIHLTNYADETI 60
DB 2 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSGRYALIHLTNYADETI 61
QY 61 SVAIDVTNVIYMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120
DB 62 SVAIDVTNVIYMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 121
QY 121 IRENIPGLPALDSAITTLFFYNANSAASALMWLIQSTSEARXYKFIHQOIGKRVDTFL 180
DB 122 IRENIPGLPALDSAITTLFFYNANSAASALMWLIQSTSEARXYKFIHQOIGKRVDTFL 181
QY 181 PSLAIISLENSWSALSKOIQIASTNNGQFESPVLINAOQRTITNVDAVVTSNIALL 240
DB 182 PSLAIISLENSWSALSKOIQIASTNNGQFESPVLINAOQRTITNVDAVVTSNIALL 241
QY 241 LNRNNMA 247
DB 242 LNRNNMA 248
XX
XX RESULT 6
XX AAB99329 standard; protein; 289 AA.
XX
XX AAB99329;
XX
XX 23-AUG-2001 (first entry)
XX
XX Trichosanthes kirilowii trichosanthin (TCS) protein sequence.
XX

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KW Trichosanthes kirilowii; trichosanthin; TCS; mutagenesis; mutation; MTCS;
XX mutant of trichosanthin; Mongolian snake-gourd; bioactivity; selectivity;
XX cancer; virus; HIV; metaphase induced labour.
XX
XX Trichosanthes kirilowii.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 230
XX FT Misc-difference 230 /note= "encoded by GCA"
XX
XX CN1283630-A.
XX
XX 14-FEB-2001.
XX
XX 02-AUG-2000; 2000CN-00119553.
XX
XX 02-AUG-2000; 2000CN-00119553.
XX
XX (SHAN-) SHANGHAI INST CYTOBIOLOGY CHINESE ACAD.
XX
XX Ke Y, Nie H;
XX
XX WPI; 2001-291745/31.
XX
XX N-PSDB; AAH41473.
XX
XX Trichosanthin mutant and its preparing process.
XX
XX Disclosure; Page 2 (disclosure); 15pp; Chinese.
XX
XX The present invention describes a trichosanthin mutant which is prepared
XX through the mutational deformation of the trichosanthin gene and using an
XX expression system. The trichosanthin gene is isolated from Trichosanthes
XX kirilowii (Mongolian snake-gourd). The trichosanthin mutant has several
XX advantages including high bioactivity, high selectivity to target, and
XX strong kill action to cancer cells, virus and HIV. It can also be used
XX for metaphase induced labour. The present sequence represents the protein
XX sequence of wild type trichosanthin which is given in the exemplification
XX of the present invention
XX
XX Sequence 289 AA;
SQ
Query Match 100.0%; Score 1221; DB 4; Length 289;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSGRYALIHLTNYADETI 60
DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSGRYALIHLTNYADETI 83
QY 61 SVAIDVTNVIYMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120
DB 64 SVAIDVTNVIYMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 143
QY 121 IRENIPGLPALDSAITTLFFYNANSAASALMWLIQSTSEARXYKFIHQOIGKRVDTFL 180
DB 122 IRENIPGLPALDSAITTLFFYNANSAASALMWLIQSTSEARXYKFIHQOIGKRVDTFL 181
QY 144 IRENIPGLPALDSAITTLFFYNANSAASALMWLIQSTSEARXYKFIHQOIGKRVDTFL 203
DB 144 IRENIPGLPALDSAITTLFFYNANSAASALMWLIQSTSEARXYKFIHQOIGKRVDTFL 203
QY 181 PSLAIISLENSWSALSKOIQIASTNNGQFESPVLINAOQRTITNVDAVVTSNIALL 240
DB 204 PSLAIISLENSWSALSKOIQIASTNNGQFESPVLINAOQRTITNVDAVVTSNIALL 263
QY 241 LNRNNMA 247
DB 264 LNRNNMA 270
XX
XX RESULT 7
XX ABB07660 standard; protein; 289 AA.
XX
XX ABB07660;
XX
XX 20-MAY-2002 (first entry)
XX

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XX		Native trichosanthin (TCS) protein sequence.
DE		
XX		Trichosanthin; TCS; mutant; MTCS; therapeutic; cytostatic; antitumour;
KW		anti-human immunodeficiency virus; virucide; immunostimulant; gene;
XV		ectopic pregnancy.
XX		
OS		Trichosanthes kirilowii.
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..23
FT	/note= "signal peptide"	
FT	Misc-difference	6
FT	/note= "encoded by GAC"	
FT	Protein	24..289
FT	/note= "mature protein"	
FT	Region	174..180
FT	/note= "MTCS contains a modification of at least one amino acid residue in this region"	
FT	Misc-difference	175
FT	/note= "encoded by ART"	
FT	Region	203..226
FT	/note= "MTCS contains a modification of at least one amino acid residue in this region"	
FT	Region	230..244
FT	/note= "MTCS contains a modification of at least one amino acid residue in this region"	
FT	Misc-difference	289
FT	/note= "encode dbv ART"	
XX		
PN	WO200212537-A2.	
XX		
PD	14-FEB-2002.	
XX		
PE	18-JUL-2001; 2001MO-CN001178.	
PR	02-AUG-2000; 2000CN-00119553.	
PR	18-JAN-2001; 2001CN-00103102.	
XX		
PA	(BEIJ-) BEIJING STM BIOTECH LTD.	
PA	(KEYY/) KE Y.	
PA	(NIEH/) NIE H.	
XX		
P1	Ke Y, Nie H;	
XX		
DR	WPI; 2002-227165/28.	
DR	N-PESDB; ABA95171.	
XX		
PT	Mutant trichosanthin protein of low antigenicity useful for treating tumor e.g. leukemia, comprises a sequence of native trichosanthin with modification of at least one amino acid residue in three specific regions.	
PT		
PS	Example 1; Fig 1; 42pp; English.	
XX		
CC	The invention relates to a mutant trichosanthin (MTCS) protein of low antigenicity comprising a sequence of native TCS with the modification of at least one amino acid residue in three regions which is' 174-180, 203-227 and 230-244 and substantially retaining the biological activities of the native TCS. The MTCS protein, its fragment or derivative is useful as an therapeutic agent; or for preparing a medicament for treating viral disease e.g. acquired immunodeficiency syndrome (AIDS), tumour e.g. leukemia, for inducing abortion and/or treating ectopic pregnancy. The present sequence represents the native TCS	
CC		
CC		
SQ	Sequence 289 AA;	
	Query Match	100.0%; Score 1221; DB 5; length 289;
	Best Local Similarity	100.0%; Pred.No.1.le-110;
	Matches 247; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 DVSRFLSGATSSGYVFISLNKALPNEKKLYDIPILRSLGSGORVALIHITNYADRTI	60

Query	Subject	Score	Length	Start	End	Ident	Score	Length	Start	End	Ident
24	DVSPFLSGATSSSYGVFISNLKALPNBRKLYDIPILRSSLPGSGRYALIHLLTNVADDTI	83	247	1	247	100	100	247	1	247	100
61	SVAILDVNTVYIMGYAGDTSYFENASATEAAKYFKAMRKVTLPSGNYERLQTAAGK	120	247	1	247	100	100	247	1	247	100
84	SVAILDVNTVYIMGYAGDTSYFENASATEAAKYFKAMRKVTLPSGNYERLQTAAGK	143	247	1	247	100	100	247	1	247	100
121	IRENIPGLPLDLSAITTLTFYNNASASALMWLLOSTSEARRYKPIEQOIGKRVKTFI	180	247	1	247	100	100	247	1	247	100
144	IRENIPGLPLDLSAITTLTFYNNASASALMWLLOSTSEARRYKPIEQOIGKRVKTFI	203	247	1	247	100	100	247	1	247	100
181	PSLAIIISLSEMSALSCKOIQIOLASTNNGGFESPVVLINAGORVTLINVDAGVTSNIAL	240	247	1	247	100	100	247	1	247	100
204	PSLAIIISLSEMSALSCKOIQIOLASTNNGGFESPVVLINAGORVTLINVDAGVTSNIAL	263	247	1	247	100	100	247	1	247	100
241	LNRRNMA 247	247	247	1	247	100	100	247	1	247	100
264	LNRRNMA 270	270	270	1	270	100	100	270	1	270	100
AA67359	AA67359 standard; protein; 247 AA.	247	247	1	247	100	100	247	1	247	100
AA67359	AA67359 standard; protein; 247 AA.	247	247	1	247	100	100	247	1	247	100
25-MAR-2003 (revised)	25-MAR-2003 (revised)	247	247	1	247	100	100	247	1	247	100
26-JUL-1995 (first entry)	26-JUL-1995 (first entry)	247	247	1	247	100	100	247	1	247	100
Trichosanthin antiviral protein.	Trichosanthin antiviral protein.	247	247	1	247	100	100	247	1	247	100
Antiviral agent; trichosanthin; HIV; hepatitis virus.	Antiviral agent; trichosanthin; HIV; hepatitis virus.	247	247	1	247	100	100	247	1	247	100
Trichosanthes kirilowii.	Trichosanthes kirilowii.	247	247	1	247	100	100	247	1	247	100
WO9426898-A1.	WO9426898-A1.	247	247	1	247	100	100	247	1	247	100
24-NOV-1994.	24-NOV-1994.	247	247	1	247	100	100	247	1	247	100
17-MAY-1994; 94WO-CN000037.	17-MAY-1994; 94WO-CN000037.	247	247	1	247	100	100	247	1	247	100
19-MAY-1993; 93CN-00112436.	19-MAY-1993; 93CN-00112436.	247	247	1	247	100	100	247	1	247	100
(SHAN-) SHANGHAI INST ORGANIC CHEM.	(SHAN-) SHANGHAI INST ORGANIC CHEM.	247	247	1	247	100	100	247	1	247	100
Chen H, Xia Y, Jiang K, Bao J;	Chen H, Xia Y, Jiang K, Bao J;	247	247	1	247	100	100	247	1	247	100
WPI, 1995-006794/01.	WPI, 1995-006794/01.	247	247	1	247	100	100	247	1	247	100
N-PSDB; AA075305.	N-PSDB; AA075305.	247	247	1	247	100	100	247	1	247	100
New genetically engineered gene for trichosanthin protein - expressed in E.coli, used to produce the protein for use as antiviral agent against HIV and hepatitis virus.	New genetically engineered gene for trichosanthin protein - expressed in E.coli, used to produce the protein for use as antiviral agent against HIV and hepatitis virus.	247	247	1	247	100	100	247	1	247	100
Claim 1; Fig 1; 37pp; Chinese.	Claim 1; Fig 1; 37pp; Chinese.	247	247	1	247	100	100	247	1	247	100
AA075305 encodes AA67359 an antiviral protein isolated from the roots of Trichosanthes kirilowii. The trichosanthin antiviral protein is useful for controlling viral infections such as HIV and hepatitis. (Updated on 25-MAR-2003 to correct PN field.)	AA075305 encodes AA67359 an antiviral protein isolated from the roots of Trichosanthes kirilowii. The trichosanthin antiviral protein is useful for controlling viral infections such as HIV and hepatitis. (Updated on 25-MAR-2003 to correct PN field.)	247	247	1	247	100	100	247	1	247	100
Sequence 247 AA;	Sequence 247 AA;	247	247	1	247	100	100	247	1	247	100
Query Match	99.8%; Score 1218; DB 2; Length 247;	247	247	1	247	100	100	247	1	247	100
Best local similarity	99.6%; Pred. No. 1.8e-110;	247	247	1	247	100	100	247	1	247	100
Matches	246; Conservative 1; Mismatches 0; Indels 0; Gaps 0	247	247	1	247	100	100	247	1	247	100
1	DVSFRLSGATSSSYGVFISNLKALPNBRKLYDIPILRSSLPGSGRYALIHLLTNVADDTI	60	247	1	247	100	100	247	1	247	100
1	DVSFRLSGATSSSYGVFISNLKALPNBRKLYDIPILRSSLPGSGRYALIHLLTNVADDTI	60	247								

```

QY      121 IRENIPLG.PALDSAITTLFFYNANSASALMWLIQSTSEAAKYFEIQOIGKRVDTFL 180
DB      121 IRENIPLG.PALDSAITTLFFYNANSASALMWLIQSTSEAAKYFEIQOIGKRVDTFL 180
QY      181 PSLAIIISLNSWSALSKQIQIASTNNQGFESPVLINQONRVITITNDAGVTSNIALL 240
DB      181 PSLAIIISLNSWSALSKQIQIASTNNQGFETPVVLINQONRVITITNDAGVTSNIALL 240
QY      241 LNRNNMA 247
DB      241 LNRNNMA 247

```

## RESULT 9

```

AAR07514
ID AAR07514 standard; protein; 289 AA.
AC AAR07514;
XX
XX
XX 06-FEB-1991 (first entry)
XX
XX Trichosanthin from Trichosanthes kirilowii.
XX Trichosanthin (TCS); Human Immunodeficiency Virus; inhibition.
XX
XX Trichosanthes kirilowii.
XX
XX Key Location/Qualifiers
XX FH 1..21
XX FT /label= "signal peptide"
XX FT /note= "hydrophobic"
XX
XX WO9012097-A.
XX
XX 18-OCT-1990.
XX
XX 04-APR-1989; 89US-0033184.
XX
XX 04-APR-1989; 89US-0033184.
XX
XX (GENE-) GENELABS INC.
XX
XX Platek M, Chow T, Fry K;
XX
XX WPI; 1990-334847/44.
XX
XX N-PSDB; AAQ06343.
XX
XX Recombinant tri:chosanthin protein - with selective inhibitory effect on
XX PT viral expression in HIV infected T-cells or monocyte-macrophase.
XX
XX Example; Fig 4; 102pp; English.
XX
XX Genomic DNA was isolated from T.kirilowii leaves from Korea and a library
XX CC was constructed. Clone pD21D was identified as likely to contain a TCS-
XX CC encoding sequence in its 4kb insert. The deduced amino acid sequence is
XX CC identical to that of TCS purified from Cantonese T.kirilowii roots,
XX CC except for 2 conservative substitu-tions, i.e. Thr for Ser at position
XX CC 211 and Met for Thr at position 224. The Canton protein lacks the last 19
XX CC C-terminal amino acid residues. See also AAQ06344-Q06351
XX
XX SQ Sequence 289 AA;

```

## Query Match

```

Best Local Similarity 99.3%; Score 1212; DB 2; Length 289;
Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 DVSFRISGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSGRYALIHLTNVDERT 60
DB      24 DVSFRISGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSGRYALIHLTNVDERT 83
QY      61 SVADIVTNVYIMGYRAGDTSYFPNEASATEAAKYVFKDAMRKVTLLPYSGNYERLQTPAAG 120

```

```

DB      84 SVADIVTNVYIMGYRAGDTSYFPNEASATEAAKYVFKDAMRKVTLLPYSGNYERLQTPAAG 143
QY      121 IRENIPLG.PALDSAITTLFFYNANSASALMWLIQSTSEAAKYFEIQOIGKRVDTFL 180
DB      144 IRENIPLG.PALDSAITTLFFYNANSASALMWLIQSTSEAAKYFEIQOIGKRVDTFL 203
QY      181 PSLAIIISLNSWSALSKQIQIASTNNQGFESPVLINQONRVITITNDAGVTSNIALL 240
DB      204 PSLAIIISLNSWSALSKQIQIASTNNQGFETPVVLINQONRVITITNDAGVTSNIALL 263
QY      241 LNRNNMA 247
DB      264 LNRNNMA 270

```

## RESULT 10

```

AAR25572
ID AAR25572 standard; protein; 289 AA.
AC AAR25572;
XX
XX
XX 25-MAR-2003 (revised)
XX DT 13-JAN-1993 (first entry)
XX
XX Trichosanthin from Trichosanthes kirilowii.
XX
XX TCS; alpha-trichosanthin; Radix trichosanthin; abortifacient;
XX KW ribosome inactivating protein; RIP; HIV-infected human T cells;
XX KW human immunodeficiency virus.
XX
XX Trichosanthes kirilowii.
XX
XX Key Location/Qualifiers
XX FH Misc-difference 57
XX FT /note= "Leu in previously published sequence"
XX FT Misc-difference 60
XX FT /note= "Ile in previously published sequence"
XX FT Misc-difference 72
XX FT /note= "Ile in previously published sequence"
XX FT Misc-difference 82..84
XX FT /note= "region not present in previously published
XX FT sequence"
XX FT Misc-difference 92..93
XX FT /note= "previously published sequence contained a 10
XX FT amino acid insert (DAGLPRNAVLI) between Val and Tyr"
XX FT Misc-difference 143
XX FT /note= "Gly in previously published sequence"
XX FT Misc-difference 144
XX FT /note= "Leu in previously published sequence"
XX FT Misc-difference 196
XX FT /note= "Ser in previously published sequence"
XX FT Misc-difference 214..215
XX FT /note= "previously published sequence contained a Leu
XX FT inserted between Ser and Trp"
XX FT Misc-difference 216
XX FT /note= "Leu in previously published sequence"
XX FT Misc-difference 231
XX FT /note= "Thr in previously published sequence"
XX FT Misc-difference 234
XX FT /note= "Ser in directly sequenced TCS"
XX FT Misc-difference 246..266
XX FT /note= "21 amino acids not present in previously
XX FT published sequence"
XX FT Misc-difference 247
XX FT /note= "Thr in directly sequenced TCS"
XX
XX US5128460-A.
XX
XX 07-JUL-1992.
XX
XX 04-APR-1990; 90US-00504775.
XX
XX 04-APR-1989; 89US-0033184.
XX
XX

```



PR 07-SEP-1989; 89US-00404326.  
 XX (GENE-) GENELABS INC.  
 XX  
 XX  
 PI Platak M, Chow TP, Fry K;  
 XX  
 DR WPI; 1992-249485/30.  
 XX N-PSDB; AAQ26499.  
 XX  
 PT Nucleic acid encoding trichosanthin protein - which can be used to  
 PT inactivate ribosome(s) to inhibit protein synthesis or to inhibit HIV  
 PT expression.

Claim 1; Fig 4; 53pp; English.

XX Trichosanthin protein was isolated from T.kirilowii root tuber and  
 CC sequenced. The amino acid sequence was used to design sets of degenerate  
 CC primers (see AAQ26506-8) for PCR amplification of the TCS coding  
 CC sequence. The amplified product was used as a probe to isolate TCS coding  
 CC sequence from T.kirilowii genomic libraries. One clone (PQ21D) contained  
 CC a 4kb insert. The amino acid sequence deduced from the PQ21D insert  
 CC differed from the purified TCS sequence by conservative substitutions at  
 CC two positions (see Features Table). The differences are postulated to  
 CC indicate minor variations between strains; the purified TCS was obtained  
 CC from the Canton region of China and the genomic DNA was obtained from  
 CC T.kirilowii leaves from Korea. The amino acid sequence was also found to  
 CC differ substantially from the previously published TCS sequence (Acta  
 CC Chemica Sinica, 43:1943, 1984 and Pure and Appl. Chem., 58(5):789, 1986).  
 CC The differences are shown in the Features Table. The present sequence  
 CC agrees closely with X-ray diffraction data on crystallized TCS. The 21-  
 CC amino acid insert also provides greater sequence homology with a number  
 CC of RIPS such as ricin A chain and abrin A chain than the previously  
 CC published sequence. (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 289 AA;

Query Match 99.3%; Score 1212; DB 2; Length 289;

Best Local Similarity 99.2%; Pred. No. 8.5e-110; Mismatches 1; Indels 0; Gaps 0;

Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSPLPSGORYALHILTNVADETI 60  
 DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSPLPSGORYALHILTNVADETI 83  
 QY 61 SVAIDVTNVIYIMGRAGDTSYFNEASATEAAKYVFKDMARKVTLPYSGYERLQTPAAGK 120  
 DB 84 SVAIDVTNVIYIMGRAGDTSYFNEASATEAAKYVFKDMARKVTLPYSGYERLQTPAAGK 143  
 QY 121 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEAAKYKFIHQIGKRVDTFL 180  
 DB 144 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEAAKYKFIHQIGKRVDTFL 203  
 QY 181 PSIAITISLNSWSALSKQIQIASTNNQGFESPVLINAOORVTTINVDAGVTSNIAL 240  
 DB 204 PSIAITISLNSWSALSKQIQIASTNNQGFETPVVLINAOORVTTINVDAGVTSNIAL 263  
 QY 241 LNNNNMA 247  
 DB 264 LNNNNMA 270

RESULT 11

AAQ29272 ID AAR29272 standard; protein; 289 AA.

XX AAR29272;

DT 25-MAR-2003 (revised)  
 DT 16-APR-1993 (first entry)

XX Trichosanthin protein (encoded by PQ21D).

KM TCS; alpha-trichosanthin; Radix-trichosanthin; primer; inhibition;  
 KM viral expression; HIV; T-cell; macrophage.  
 XX  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Peptide 1..23  
 FT Peptide /label= sig peptide  
 FT /note= "putative N-terminal extension of the mature TCS"

FT Protein 24..270  
 FT /label= mat\_protein  
 FT /note= "plant-derived TCS has Ser at this position"

FT Misc-difference 247  
 FT /note= "plant-derived TCS has Thr at this position"

FT Protein 270..289  
 FT /note= "putative C-terminal extension of the mature TCS"

PN US5166056-A.

PD 24-NOV-1992.

PF 09-DEC-1991; 91US-00804293.

PR 04-APR-1989; 89US-00331184.  
 PR 07-SEP-1989; 89US-00404326.

PA (GENE-) GENELABS INC.

PI Platak M, Chow TP;

DR WPI; 1992-414954/50.

XX Recombinant Trichosanthin protein prodn. in E. coli - for use in the  
 PT selective inhibition of viral expression in HIV infected cells.

XX Disclosure; Fig 4; 37pp; English.

XX The sequence is identical to that of plant-derived TCS except for two  
 CC conservative changes: a Thr for a Ser substitution at position 21 and a  
 CC Met for a Thr substitution at position 224. TCS is likely produced as a  
 CC secreted protein that undergoes post-translational processing at both the  
 CC amino and carboxy ends. The TCS coding sequence was amplified using the  
 CC primers of AAQ31828-30. The amplified prod. has the sequence of AAQ31827,  
 CC which was used as a probe. One isolate, PQ21D, comprises the sequence of  
 CC AAQ31826. The recombinant TCS sequence may be used in the recombinant  
 CC prodn. of TCS. TCS can be used for the selective inhibition of viral  
 CC expression in HIV-infected human T-cells or macrophages. (Updated on 25-  
 MAR-2003 to correct PF field.)

XX Sequence 289 AA;

Query Match 99.3%; Score 1212; DB 2; Length 289;

Best Local Similarity 99.2%; Pred. No. 8.5e-110; Mismatches 1; Indels 0; Gaps 0;

Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSPLPSGORYALHILTNVADETI 60  
 DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSPLPSGORYALHILTNVADETI 83  
 QY 61 SVAIDVTNVIYIMGRAGDTSYFNEASATEAAKYVFKDMARKVTLPYSGYERLQTPAAGK 120  
 DB 84 SVAIDVTNVIYIMGRAGDTSYFNEASATEAAKYVFKDMARKVTLPYSGYERLQTPAAGK 143  
 QY 121 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEAAKYKFIHQIGKRVDTFL 180  
 DB 144 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEAAKYKFIHQIGKRVDTFL 203  
 QY 181 PSIAITISLNSWSALSKQIQIASTNNQGFESPVLINAOORVTTINVDAGVTSNIAL 240  
 DB 204 PSIAITISLNSWSALSKQIQIASTNNQGFETPVVLINAOORVTTINVDAGVTSNIAL 263  
 QY 241 LNNNNMA 247

Db 264 LNRNMA 270

## RESULT 12

AAR32986  
ID AAR32986 standard; protein; 289 AA.

AC AAR32986;  
XX  
XX 27-AUG-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 17-JUN-1993 (first entry)

DE Encodes chinese cucumber alpha-tricosanthin.

XX  
XX Recombinant products; commercial production; fermentation; biosynthesis;  
KM natural products; recombinant proteins; product expression;  
KW protein expression; expressed proteins.

OS Cucurbitaceae.

PN MO3033161-A1.

PD 18-FEB-1993.

PF 31-JUL-1992; 92WC-US006359.

XX 01-AUG-1991; 91US-00739143.

XX (DONS/) DONSON J.

PA (DAWS/) DAWSON W O.

PA (GRAN/) GRANTHAM G L.

PA (TURP/) TURPEN T H.

PA (GARG/) GARGER S J.

PA (GRIL/) GRILLE L K.

XX Donson J, Dawson WO, Granttham GL, Turpen TH, Turpen AM;

PI Garger SJ, Grille LK;

XX WPI, 1993-076518/09.

DR N-PSDB; AAQ37679.

XX Recombinant plant viral nucleic acids - used to express a prod., e.g.

PT antibody or IL-1 in a plant.

XX Example 4; Page 96; 30pp; English.

XX This sequence represents chinese cucumber alpha-tricosanthin. The coding

CC sequence is inserted into a recombinant plant viral nucleic acid which is

CC then used to express a recombinant product (in this case alpha-

CC tricosanthin) in a plant. The plant viral sequence may be from tobacco

CC mosaic, cucumber green mottle, cowpea mosaic, brome mosaic, broad bean

CC mottle, rice necrosis, geminiviruses, tomato golden mosaic, Cassava

CC latent and maize streak viruses. (Updated on 25-MAR-2003 to correct PN

CC field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-

XX 2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 289 AA;

XX

Query Match 99.3%; Score 1212; DB 2; Length 289;

Best Local Similarity 99.2%; Pred. No. 8-5e-110; Indels 0; Gaps 0;

Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFINLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 60

Db 24 DVSFRLSGATSSSYGVFINLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 83

QY 61 SVADIVTNVYINGYRAGDTSYFPNEASATEAAKYVKDMARKTLPYSGNYERLQTAAGK 120

Db 84 SVADIVTNVYINGYRAGDTSYFPNEASATEAAKYVKDMARKTLPYSGNYERLQTAAGK 143

QY 121 IRENIPLGLPALSATITLTFYNNANSASALMWLIQSTSEARARYKFEQIGKRVDTFL 180

Db 144 IRENIPLGLPALSATITLTFYNNANSASALMWLIQSTSEARARYKFEQIGKRVDTFL 203

QY 181 PSLATISLENSWSALSKQIQIASTNNQFESRPLYLINONQRYVTITNDAGVTSNIAL 240

Db 204 PSLATISLENSWSALSKQIQIASTNNQFETPVVLINONQRYVTITNDAGVTSNIAL 263

QY 241 LNRNMA 247

Db 264 LNRNMA 270

## RESULT 13

AAR55129  
ID AAR55129 standard; protein; 289 AA.

AC AAR55129;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 11-JAN-1995 (first entry)

XX Alpha-trichosanthen coding.

XX Virus; recombinant; plant virus; alpha trichosanthen; phenotype;

KW alpha amylase; alpha haemoglobin; brome mosaic virus; gemini virus;

KW rice necrosis virus tobamovirus; gene expression; chinese cucumber.

XX Trichosanthes kirilowii.

XX US5316931-A.

XX 31-MAY-1994.

XX 31-JUL-1992; 92US-00923692.

XX 26-FEB-1988; 88US-00160766.

XX 26-FEB-1988; 88US-00160771.

XX 15-JUL-1988; 88US-00219279.

XX 17-FEB-1988; 88US-00310881.

XX 05-MAY-1989; 89US-00347637.

XX 08-JUN-1989; 89US-00363138.

XX 22-OCT-1990; 90US-00600244.

XX 16-JAN-1991; 91US-00641617.

XX 26-JUL-1991; 91US-00737899.

XX 01-AUG-1991; 91US-00739143.

XX (BIOS-) BIOSOURCE GENETICS CORP.

XX Garger SJ, Turpen AM, Grille LK, Granttham GL, Dawson WO, Donson J;

PI Turpen TH;

XX WPI, 1994-176269/21.

DR N-PSDB; AAQ65573.

XX New recombinant plant viral nucleic acid - capable of systemic infection

PT and stable expression of non-native nucleic acid in plant host.

XX Example 4; Col 47-50; 44pp; English.

XX The alpha-trichosanthen gene may be inserted into a recombinant plant

CC virus which can then be used to infect plants for the production of non-

CC native products (in this case alpha-trichosanthen). Other genes which

CC may be inserted into the virus are those which control a phenotypic

CC trait, such as male sterility, or sequences encoding anti-sense RNA which

CC can be useful to prevent the expression of undesired phenotypic traits.

CC The recombinant virus is derived from a plus sense, single stranded virus

CC selected from tobamovirus, brome mosaic virus, rice necrosis virus or a

CC gemini virus. (Updated on 25-MAR-2003 to correct PF field.) (Updated on

XX 27-AUG-2003 to correct OS field.)

XX Sequence 289 AA;

Query Match 99.3%; Score 1212; DB 2; Length 289;  
 Best Local Similarity 99.2%; Pred. No. 8.5e-110;  
 Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSLSPGSOYALIHITNVADETI 60  
 DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSLSPGSOYALIHITNVADETI 83  
 QY 61 SVADVTNVIYIMGYRAGDTSYFFNEASATEAAKYVKDMARKYTLPSYSGYERLQTPACK 120  
 DB 84 SVADVTNVIYIMGYRAGDTSYFFNEASATEAAKYVKDMARKYTLPSYSGYERLQTPACK 143  
 QY 121 IRENIPILGLPALDSATITLTFYNNANSASALMWLIQSTSEAAKYKFEIOQIGKRVDTFL 180  
 DB 144 IRENIPILGLPALDSATITLTFYNNANSASALMWLIQSTSEAAKYKFEIOQIGKRVDTFL 203  
 QY 181 PSIAITSLSENSWALSQKQIQIASTNNQGFESPVVLIINAQNRVTITNVDAVVTSNIAL 240  
 DB 204 PSIAITSLSENSWALSQKQIQIASTNNQGFETPVVLIINAQNRVTITNVDAVVTSNIAL 263  
 QY 241 LNRRNMA 247  
 DB 264 LNRRNMA 270

RESULT 14  
 AAM10468  
 ID AAM10468 standard; protein; 289 AA.  
 AC AAM10468;  
 XX  
 XX 17-OCT-2003 (revised)  
 DT 26-APR-1997 (first entry)  
 XX  
 DE Chinese cucumber alpha-trichosanthin.  
 KW Recombinant viral nucleic acid; RNA virus; vector; tobacco mosaic virus;  
 KM TMV; Chinese cucumber; alpha-trichosanthin;  
 KW ribosome inactivating protein; antiviral; virucide; transgenic plant.  
 XX  
 OS Trichosanthes kirilowii; Maximowicz.  
 XX  
 XX WO9640867-A1.  
 PN 19-DEC-1996.  
 PD  
 XX  
 PF 06-JUN-1996; 96WO-US009299.  
 XX  
 PR 07-JUN-1995; 95US-00483502.  
 XX  
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.  
 XX  
 PI Donson J, Dawson WO, Grantham GL, Turpen TH, Turpen AM;  
 PI Garger SJ, Grill LK;  
 XX  
 DR WPI; 1997-065181/06.  
 DR N-PSDB; AAT47094.  
 XX  
 PT Recombinant viral nucleic acid producing, e.g. male sterility in plants -  
 PT comprises nucleic acid whose transcription is controlled by another  
 PT sequence.  
 PT  
 XX  
 XX Example 4; Page 124-125; 149pp; English.  
 XX  
 CC Chinese cucumber alpha-trichosanthin (AAM10468) is a ribosome  
 CC inactivating protein of potential use in the treatment of HIV infection.  
 CC  
 CC Expression vector pBCG152 was constructed in which the alpha-  
 CC trichosanthin coding sequence (see also AAT47094) was placed under  
 CC control of the promoter of the tobacco mosaic virus-U1 coat protein gene,  
 CC which had been deleted. The viral nucleic acid was capable of self-  
 CC replication, encapsidation and systemic spread in infected Nicotiana  
 CC benthamiana plants, and directed the high-level expression of

CC biologically active alpha-trichosanthin in plant tissues. (Updated on 17-  
 CC OCT-2003 to standardise OS field)  
 CC  
 CC OCT-2003 to standardise OS field)  
 CC  
 CC Sequence 289 AA;  
 SQ

Query Match 99.3%; Score 1212; DB 2; Length 289;  
 Best Local Similarity 99.2%; Pred. No. 8.5e-110;  
 Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSLSPGSOYALIHITNVADETI 60  
 DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSLSPGSOYALIHITNVADETI 83  
 QY 61 SVADVTNVIYIMGYRAGDTSYFFNEASATEAAKYVKDMARKYTLPSYSGYERLQTPACK 120  
 DB 84 SVADVTNVIYIMGYRAGDTSYFFNEASATEAAKYVKDMARKYTLPSYSGYERLQTPACK 143  
 QY 121 IRENIPILGLPALDSATITLTFYNNANSASALMWLIQSTSEAAKYKFEIOQIGKRVDTFL 180  
 DB 144 IRENIPILGLPALDSATITLTFYNNANSASALMWLIQSTSEAAKYKFEIOQIGKRVDTFL 203  
 QY 181 PSIAITSLSENSWALSQKQIQIASTNNQGFESPVVLIINAQNRVTITNVDAVVTSNIAL 240  
 DB 204 PSIAITSLSENSWALSQKQIQIASTNNQGFETPVVLIINAQNRVTITNVDAVVTSNIAL 263  
 QY 241 LNRRNMA 247  
 DB 264 LNRRNMA 270

RESULT 15  
 AAM11870  
 ID AAM11870 standard; protein; 289 AA.  
 AC AAM11870;  
 XX  
 XX 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 21-APR-1997 (first entry)  
 XX  
 DE Chinese cucumber alpha-trichosanthin.  
 KW Recombinant virus; alpha-haemoglobin; human; chinese cucumber;  
 KM alpha-trichosanthin; rice; alpha amylase; beta-haemoglobin;  
 KW subgenomic promoter; coat protein.  
 XX  
 OS Cucumis sp.  
 XX  
 PN US5589367-A.  
 XX  
 PD 31-DEC-1996.  
 XX  
 PF 19-JAN-1994; 94US-00184237.  
 XX  
 PR 26-FEB-1988; 88US-00160766.  
 PR 26-FEB-1988; 88US-00160771.  
 PR 15-JUL-1988; 88US-00219279.  
 PR 17-FEB-1989; 89US-00310881.  
 PR 05-MAY-1989; 89US-00347637.  
 PR 08-JUN-1989; 89US-00363138.  
 PR 22-OCT-1990; 90US-00600244.  
 PR 16-JAN-1991; 91US-00641617.  
 PR 26-JUL-1991; 91US-00737899.  
 PR 01-AUG-1991; 91US-00739143.  
 PR 31-JUL-1992; 92US-00923692.  
 XX  
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.  
 XX  
 PI Garger SJ, Turpen AM, Grill LK, Grantham GL, Donson J, Dawson WO;  
 PI Turpen TH;  
 XX  
 DR WPI; 1997-076845/07.  
 DR N-PSDB; AAT61376.

XX Recombinant viral DNA for altering plant phenotype or protein prodn -  
 PT contains non-native sub-genomic promoter for expression of heterologous  
 PR protein and native promoter for expression of coat protein.  
 XX

PS Example 4; Col 45-46; 42pp; English.

CC The sequences given in AM11868-71 represent proteins which were produced  
 CC by the recombinant viruses of the invention. The viruses are recombinant  
 CC plant viruses which comprise a native plant virus subgenomic promoter, at  
 CC least one non-native plant virus subgenomic promoter, and a sequence  
 CC encoding a plant virus coat protein. These heterologous sequences are  
 CC preferably under the control of the native promoter sequence. By using a  
 CC plant virus existing cells can be altered with a new coding sequences  
 CC without involving germ cell. The recombinant viruses are stable and can  
 CC cause systemic infection, with stable expression/transcription in plants  
 CC that are hosts for the non-native part of the vector. The nucleotide  
 CC sequences encoding these protein preferably integrated in plant viruses  
 CC having either the O-coat protein or the UI-coat protein gene. (Updated on  
 CC 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR  
 CC field.) (Updated on 27-AUG-2003 to correct OS field.)  
 XX

SQ Sequence 289 AA;

Query Match 99.3%; Score 1212; DB 2; Length 289;

Best Local Similarity 99.2%; Pred. No. 8.5e-110;

Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRISGATSSSYGVFISNLRKALPNERKYDIPILRSSLPQSGRYALIHITNVADETI 60  
 |||||  
 DB 24 DVSFRISGATSSSYGVFISNLRKALPNERKYDIPILRSSLPQSGRYALIHITNVADETI 83  
 |||||  
 QY 61 SVAIDVTNYINGYRAGDTSYFENEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120  
 |||||  
 DB 84 SVAIDVTNYINGYRAGDTSYFENEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAAGK 143  
 |||||  
 QY 121 IRENIPUGLPALDSAITTLFFYNANSAASALMWLIQSTSEAAKYKPIEQQIGKRVDTFL 180  
 |||||  
 DB 144 IRENIPUGLPALDSAITTLFFYNANSAASALMWLIQSTSEAAKYKPIEQQIGKRVDTFL 203  
 |||||  
 QY 181 PSLAIIISLNSWSALSQIQIASTNNGQESPVLINAONORTITNVDAVVTISNIALL 240  
 |||||  
 DB 204 PSLAIIISLNSWSALSQIQIASTNNGQESPVLINAONORTITNVDAVVTISNIALL 263  
 |||||  
 QY 241 INRNMMMA 247  
 |||||  
 DB 264 INRNMMMA 270  
 |||||

Search completed: April 12, 2005, 15:10:00  
 Job time : 112.519 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: April 12, 2005, 14:57:02 ; Search time 25.3451 Seconds  
(without alignment)

937.676 Million cell updates/sec

Title: US-09-905-247A-8

Perfect score: 1221

Sequence: 1 DVSPRLSGATSSSYGVFIN.....VDAGVTSNIALILRNMA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pirl:\*  
2: pirl:\*  
3: pirl:\*  
4: pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1221	100.0	289	1 RLITZT	rRNA N-glycosidase
2	1194	97.8	247	2 JU0393	karsaurin - Mongol
3	1194	97.8	289	2 JCS606	karsaurin C - Tric
4	1189	97.4	247	2 JCS032	karsaurin-B - Tric
5	802	65.7	286	1 RLPIGC	rRNA N-glycosidase
6	754	61.8	277	2 S22494	rRNA N-glycosidase
7	728.5	59.7	286	2 S23519	beta-luffin - smoo
8	709	58.1	286	2 S25560	rRNA N-glycosidase
9	706	57.8	286	2 JCS435	rRNA N-glycosidase
10	680	55.7	250	2 JN0108	luffin-B - smooth
11	665.5	54.6	245	2 JCS480	rRNA N-glycosidase
12	421	34.5	576	1 RLCSAG	ricin D precursor
13	396.5	32.5	564	1 RLCSAG	agglutinin precurs
14	352	28.8	521	2 C39761	abrin (clone 7.2)
15	343	28.1	528	2 S32431	abrin-d precursor
16	343	28.1	562	2 S16022	abrin-c precursor
17	340.5	27.9	527	2 S32430	abrin-b precursor
18	336	27.5	528	1 TZLSA	abrin-a precursor
19	335.5	27.5	570	2 S62627	agglutinin I precu
20	325	26.6	254	2 PD0018	mistletoe lectin I
21	321	26.3	316	2 JTO753	rRNA N-glycosidase
22	266.5	21.8	272	2 JCS481	betanulin - beet
23	261	21.4	313	2 S17757	rRNA N-glycosidase
24	258.5	21.2	294	2 S28421	rRNA N-glycosidase
25	240.5	19.7	261	2 UEO401	antiviral protein
26	190.5	15.6	310	2 S46239	ribosome-inactivat
27	187	15.3	278	2 A39817	rRNA N-glycosidase
28	169.5	13.9	289	2 T12573	rRNA N-glycosidase
29	168	13.8	45	2 A39598	TAP-29 anti-HIV pr

30	163.5	13.4	253	2 S28542	rRNA N-glycosidase
31	163.5	13.4	253	2 A58923	rRNA N-glycosidase
32	162.5	13.3	253	2 S28539	rRNA N-glycosidase
33	159.5	13.1	253	2 S28541	rRNA N-glycosidase
34	158.5	13.0	283	2 S05205	rRNA N-glycosidase
35	157.5	12.9	292	1 RLQHG2	rRNA N-glycosidase
36	156.5	12.8	293	2 S29931	rRNA N-glycosidase
37	155	12.7	253	2 S17519	rRNA N-glycosidase
38	153	12.5	43	2 S16491	rRNA N-glycosidase
39	142.5	11.7	236	2 S17932	rRNA N-glycosidase
40	140.5	11.5	106	2 B39761	abrin (clone 3.7)
41	122	10.0	280	1 RLBI	rRNA N-glycosidase
42	119	9.7	280	2 JCS848	protein synthesis
43	118	9.7	281	2 B38664	30k ribosome inact
44	111.5	9.1	319	2 T76713	variant shiga-like
45	111.5	9.1	319	2 S58343	Shiga-like toxin I

## ALIGNMENTS

## RESULT 1

RLITZT  
rRNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian  
N/Alternate names: alpha-TCS; type I ribosome-inactivating protein  
C/Species: Trichosanthes kirilowii (Mongolian snake-gourd)  
C/Date: 30-Sep-1988 #sequence revision 26-Jan-1996 #text change 09-Jul-2004  
C/Accession: JTO566; A36274; JCI093; A36273; JTO003  
R/Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W.  
Gene 97, 267-272, 1991  
A>Title: Cloning of trichosanthin cDNA and its expression in Escherichia coli.  
A/Reference number: JTO566; MUID:91153657; PMID:1899291  
A/Accession: JTO566  
A/Molecule type: mRNA  
A/Residues: 1-289 <SHA>  
A/Cross-references: UNIPROT:P09989; GB:M34858; NID:G170536; PIDN:AAA4207.1; PID:G170537  
A/Experimental source: tuber  
R/Chow, T.P.; Feldman, R.R.; Lovett, M.; Platak, M.  
J. Biol. Chem. 265, 8670-8674, 1990  
A>Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I rhl  
A/Reference number: A36274; MUID:90256790; PMID:2341400  
A/Accession: A36274  
A/Molecule type: DNA  
A/Residues: 1-233, 'T', 235-246, 'W', 248-289 <CHO>  
A/Cross-references: GB:J05434; NID:G170534; PIDN:AAA34206.1; PID:G170535  
R/Cheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.  
Acta Genet. Sin. 21, 42-51, 1994  
A>Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.  
A/Reference number: JCI093; MUID:94271613; PMID:8003348  
A/Accession: JCI093  
A/Molecule type: DNA  
A/Residues: 1-77, 'V', 74-90, 'S', 92-233, 'T', 235-267, 'D', 269-289 <ZHE>  
A/Cross-references: GB:S70176; NID:G547148; PIDN:AAA31048.1; PID:G547149  
R/Collins, E.J.; Roberts, J.D.; Lofrest, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwar  
J. Biol. Chem. 265, 8665-8669, 1990  
A>Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abri  
A/Reference number: A36273; MUID:90256789; PMID:2341399  
A/Accession: A36273  
A/Molecule type: protein  
A/Residues: 24-270 <COL>  
R/Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Y.  
Pure Appl. Chem. 58, 789-798, 1996  
A>Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application  
A/Reference number: JTO003  
A/Accession: JTO003  
A/Molecule type: protein  
A/Residues: 24-56, 'L', 58-59, 'I', 61-71, 'I', 73-81, 85-86, 'L', 88-92, 'DAGLPNAV', 93-142, 'GL'  
R/Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
submitted to the Brookhaven Protein Data Bank, July 1994  
A/Reference number: A67091; PDB:1MRJ  
A/Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-  
R/Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.

submitted to the Brookhaven Protein Data Bank, July 1994  
A:Reference number: A67092; PDB:1MRK  
A:Contents: annotation; X-ray crystallography, 1.6 angstroms, with formycin, residues 24  
R:Xiong, J.P.; Xia, Z.X.; Wang, Y.  
Submitted to the Brookhaven Protein Data Bank, December 1994  
A:Reference number: A66711; PDB:1TCS  
A:Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27  
R:Xiong, J.P.; Xia, Z.X.; Wang, Y.  
Nat. Struct. Biol. 1, 695-700, 1994  
A:Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re  
A:Reference number: A56822; PMID:95360714; PMID:7534073  
A:Contents: annotation; X-ray crystallography, 1.7 angstroms  
A:Comment: Alpha-trichosanthin has been used to induce abortions.  
C:Genetics:  
A:Gene: tcs  
C:Function:  
A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA then  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: abortifacient; glycosidase; hydrolase; root; toxin  
F:1-23/Domain: signal sequence #status predicted <Sig>  
F:24-270/Product: trichosanthin alpha #status experimental <Mat>  
F:27-266/Domain: rRNA N-glycosidase homology <RNG>  
F:271-289/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F:93,183,186/Active site: Tyr, Glu, Arg #status predicted

Query Match 100.0%; Score 1221; DB 1; Length 289;  
Best Local Similarity 100.0%; Pred. No. 3; 7e-95;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSPGSQRYALIHLTNYADETI 60  
DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSPGSQRYALIHLTNYADETI 83  
QY 61 SVAIDVTNYVIMGYRAGDTSYFFNEASATEAKYFKDMRKVTLPYSGNVERLQTAAGK 120  
DB 84 SVAIDVTNYVIMGYRAGDTSYFFNEASATEAKYFKDMRKVTLPYSGNVERLQTAAGK 143  
QY 121 IRENIPPLGLPALSATITLTFYNNANSASALMWLQSTSEARRYKFEIQIGKRVDTKL 180  
DB 144 IRENIPPLGLPALSATITLTFYNNANSASALMWLQSTSEARRYKFEIQIGKRVDTKL 203  
QY 181 PSLAIIISLNSWSALSKOIQIASTNNGOFESPVLINQONRVTTTNVDAGVTSNIALL 240  
DB 204 PSLAIIISLNSWSALSKOIQIASTNNGOFESPVLINQONRVTTTNVDAGVTSNIALL 263  
QY 241 LNRNNMA 247  
DB 264 LNRNNMA 270

## RESULT 2

karasurin - Mongolian snake-gourd  
C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: J00393; P0163  
R:Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y.  
Chem. Pharm. Bull. 39, 1244-1249, 1991  
A:Title: The complete amino acid sequence of an abortifacient protein, karasurin.  
A:Reference number: J00393; PMID:92005921; PMID:1914000  
A:Accession: J00393  
A:Molecule type: protein  
A:Residues: 1-247 <TOY>  
A:Cross-references: UNIPROT:P24478  
A:Note: a sequence which lacks Ala-247 is also shown in this publication  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: abortifacient  
F:4-243/Domain: rRNA N-glycosidase homology <RNG>

Query Match 97.8%; Score 1194; DB 2; Length 247;  
Best Local Similarity 97.6%; Pred. No. 5; 5e-93;  
Matches 241; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSPGSQRYALIHLTNYADETI 60  
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSPGSQRYALIHLTNYADETI 60  
QY 61 SVAIDVTNYVIMGYRAGDTSYFFNEASATEAKYFKDMRKVTLPYSGNVERLQTAAGK 120  
DB 61 SVAIDVTNYVIMGYRAGDTSYFFNEASATEAKYFKDMRKVTLPYSGNVERLQTAAGK 120  
QY 121 IRENIPPLGLPALSATITLTFYNNANSASALMWLQSTSEARRYKFEIQIGKRVDTKL 180  
DB 121 IRENIPPLGLPALSATITLTFYNNANSASALMWLQSTSEARRYKFEIQIGKRVDTKL 180  
QY 181 PSLAIIISLNSWSALSKOIQIASTNNGOFESPVLINQONRVTTTNVDAGVTSNIALL 240  
DB 181 PSLAIIISLNSWSALSKOIQIASTNNGOFESPVLINQONRVTTTNVDAGVTSNIALL 240  
QY 241 LNRNNMA 247  
DB 241 LNRNNMA 247

## RESULT 3

JC5606  
karasurin C - Trichosanthes kirilowii var. japonica  
N:Contains: karasurin A  
C:Species: Trichosanthes kirilowii var. japonica  
C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 09-Jul-2004  
C:Accession: JC5606; JC5033  
R:Mizukami, H.; Iida, K.; Kondo, T.; Ogihara, Y.  
Biol. Pharm. Bull. 20, 711-713, 1997  
A:Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating prote  
A:Reference number: JC5606; PMID:97356562; PMID:9212998  
A:Accession: JC5606  
A:Molecule type: DNA  
A:Residues: 1-289 <MI2>  
A:Cross-references: UNIPROT:P24478; DDBJ:AB000666; NID:92329830; PIDN:BAA21786.1; PID:92  
R:Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.  
Biol. Pharm. Bull. 19, 1485-1489, 1996  
A:Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka  
A:Reference number: JC5032; PMID:97108848; PMID:8951169  
A:Accession: JC5033  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 22-270 <KON>  
C:Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
F:22-270/Product: karasurin C #status predicted <MAC>  
F:24-270/Product: karasurin A #status predicted <MAA>  
F:27-266/Domain: rRNA N-glycosidase homology <RNG>

Query Match 97.8%; Score 1194; DB 2; Length 289;  
Best Local Similarity 97.6%; Pred. No. 6; 9e-93;  
Matches 241; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSPGSQRYALIHLTNYADETI 60  
DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSPGSQRYALIHLTNYADETI 83  
QY 61 SVAIDVTNYVIMGYRAGDTSYFFNEASATEAKYFKDMRKVTLPYSGNVERLQTAAGK 120  
DB 84 SVAIDVTNYVIMGYRAGDTSYFFNEASATEAKYFKDMRKVTLPYSGNVERLQTAAGK 143  
QY 121 IRENIPPLGLPALSATITLTFYNNANSASALMWLQSTSEARRYKFEIQIGKRVDTKL 180  
DB 144 IRENIPPLGLPALSATITLTFYNNANSASALMWLQSTSEARRYKFEIQIGKRVDTKL 203  
QY 181 PSLAIIISLNSWSALSKOIQIASTNNGOFESPVLINQONRVTTTNVDAGVTSNIALL 240  
DB 204 PSLAIIISLNSWSALSKOIQIASTNNGOFESPVLINQONRVTTTNVDAGVTSNIALL 263  
QY 241 LNRNNMA 247  
DB 241 LNRNNMA 247

Db 264 LNENMMA 270

RESULT 4

UC5032  
karasurin-B - Trichosanthes kirilowii var. japonica  
C/Species: Trichosanthes kirilowii var. japonica  
C/Date: 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C/Accession: JCS032  
R/Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.  
Biol. Pharm. Bull. 19, 1485-1489, 1996  
A/Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka  
A/Reference number: JCS032; PMID:97108848; PMID:8951169  
A/Accession: JCS032  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-247 <KON>  
A/Cross-references: UNIPROT:Q41216; UNIPROT:Q94KE4; UNIPROT:O8LPV7  
C/Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyze  
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
F/4-243/Domain: rRNA N-glycosidase homology <RNG>

Query Match 97.4%; Score 1189; DB 2; Length 247;  
Best Local Similarity 97.2%; Pred. No. 1.5e-92;  
Matches 240; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSGYGFISMLRKALPNERKLYDIPILRSSLPQSQRVALHILNVADETI 60  
Db 1 DVSFRLSGATSSGYGFISMLRKALPNERKLYDIPILRSSLPQSQRVALHILNVADETI 60

QY 61 SVADVTNVIYMGVAGDTSYFPEEASATEAKYVFDARKYTLPPSGNYERLQTAAGK 120  
Db 61 SVADVTNVIYMGVAGDTSYFPEEASATEAKYVFDARKYTLPPSGNYERLQTAAGK 120

QY 121 IRENIPILGIPALDSATITLTFYNNANSAASALMVLIOSTSEAAKYEIOIGKRVDTFL 180  
Db 121 IRENIPILGIPALDSATITLTFYNNANSAASALMVLIOSTSEAAKYEIOIGKRVDTFL 180

QY 121 IRENIPILGIPALDSATITLTFYNNANSAASALMVLIOSTSEAAKYEIOIGKRVDTFL 180  
Db 121 IRENIPILGIPALDSATITLTFYNNANSAASALMVLIOSTSEAAKYEIOIGKRVDTFL 180

QY 181 PSIAITISLENSWGLSKQIOIASTNNGQFSPVLLINAQORVTITNVDAVGTSTNIAL 240  
Db 181 PSIAITISLENSWGLSKQIOIASTNNGQFSPVLLINAQORVTITNVDAVGTSTNIAL 240

QY 241 LNENMMA 247  
Db 241 LNENMMA 247

RESULT 5

R/PUGG  
rRNA N-glycosidase (EC 3.2.2.22) alpha-momorcharin precursor [validated] - balsam pear  
N/Alternate names: agglutinin; momordin-A; ribosome-inactivating protein momorcharin alif  
C/Species: Momordica charantia (balsam pear, bitter melon)  
C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C/Accession: S14273; A61318; S16490; JN0628; S01670  
R/Ho, W.K.K.; Liu, S.C.; Shaw, P.C.; Yeung, H.W.; Ng, T.B.; Chan, W.Y.  
Biochim. Biophys. Acta 1088, 311-314, 1991  
A/Title: Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating protein.  
A/Reference number: S14273; PMID:91159486; PMID:2001404  
A/Accession: S14273  
A/Molecule type: mRNA  
A/Residues: 1-286 <HOW>  
A/Cross-references: UNIPROT:P16094; EMBL:X57682; NID:G19527; PIDD:CAA40869.1; PIDD:G19528  
R/Hil, S.S.L.  
Experientia 36, 524-527, 1980  
A/Title: Purification and partial characterization of two lectins from Momordica charant  
A/Reference number: A61318; PMID:80201763; PMID:7379938  
A/Accession: A61318  
A/Molecule type: protein  
A/Residues: 24-50 <LUA>  
A/Note: as a lectin shows agglutinating activity for type-O red blood cells  
R/Montecuch, P.C.; Lazzerini, A.M.; Barbieri, L.; Stipre, F.; Sorita, M.; Lappi, D.  
Int. J. Pept. Protein Res. 33, 263-267, 1989  
A/Title: N-terminal sequence of some ribosome-inactivating proteins.

A/Reference number: S16331; PMID:89326691; PMID:2753596  
A/Accession: S16490  
A/Molecule type: protein  
A/Residues: 24-68, 'X', '70' <MON>  
R/Minami, Y.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 57, 1141-1144, 1993  
A/Title: The complete amino acid sequence of momordin-a, a ribosome-inactivating protei  
A/Reference number: JN0628; PMID:93372465; PMID:7763984  
A/Accession: JN0628  
A/Molecule type: protein  
A/Residues: 24-107, 'Q', '109', '123', '125', '147', 'L', '149', '154', 'I', '156', '205', 'I', '207', '208', 'L', '210', '214',  
A/Experimental source: seed  
R/Ren, J.; Wang, Y.; Dong, Y.; Stuart, D.I.  
submitted to the Brookhaven Protein Data Bank, January 1994  
A/Reference number: A52272; PDB:1MHC  
A/Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 24-269  
R/Husain, J.; Tickle, I.J.; Wood, S.P.  
submitted to the Brookhaven Protein Data Bank, March 1994  
A/Reference number: A52385; PDB:1MOM  
A/Contents: annotation; X-ray crystallography, 2.16 angstroms, residues 24-86, 'L', '88-26  
R/Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.  
submitted to the Brookhaven Protein Data Bank, July 1994  
A/Reference number: A67089; PDB:1MRH  
A/Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 24-77, 'R', '79-132  
C/Function:  
A/Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA the  
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C/Keywords: glycoprotein; glycosidase; hydrolase; lectin; seed; toxin  
F/1-18/Domain: signal sequence #status predicted <SIG>  
F/19-23/Domain: amino-terminal propeptide #status predicted <PRO>  
F/24-269/Product: rRNA N-glycosidase alpha-momorcharin #status experimental <MAT>  
F/270-286/Domain: rRNA N-glycosidase homology <RNG>  
F/293,183,186/Active site: Tyr, Glu, Arg #status predicted  
F/250/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 65.7%; Score 802; DB 1; Length 286;  
Best Local Similarity 65.2%; Pred. No. 6.1e-60;  
Matches 161; Conservative 37; Mismatches 49; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSGYGFISMLRKALPNERKLYDIPILRSSLPQSQRVALHILNVADETI 60  
Db 24 DVSFRLSGATSSGYGFISMLRKALPNERKLYDIPILRSSLPQSQRVALHILNVADETI 60

QY 61 SVADVTNVIYMGVAGDTSYFPEEASATEAKYVFDARKYTLPPSGNYERLQTAAGK 120  
Db 61 SVADVTNVIYMGVAGDTSYFPEEASATEAKYVFDARKYTLPPSGNYERLQTAAGK 120

QY 121 IRENIPILGIPALDSATITLTFYNNANSAASALMVLIOSTSEAAKYEIOIGKRVDTFL 180  
Db 121 IRENIPILGIPALDSATITLTFYNNANSAASALMVLIOSTSEAAKYEIOIGKRVDTFL 180

QY 121 IRENIPILGIPALDSATITLTFYNNANSAASALMVLIOSTSEAAKYEIOIGKRVDTFL 180  
Db 121 IRENIPILGIPALDSATITLTFYNNANSAASALMVLIOSTSEAAKYEIOIGKRVDTFL 180

QY 181 PSIAITISLENSWGLSKQIOIASTNNGQFSPVLLINAQORVTITNVDAVGTSTNIAL 240  
Db 181 PSIAITISLENSWGLSKQIOIASTNNGQFSPVLLINAQORVTITNVDAVGTSTNIAL 240

QY 204 PSIAITISLENSWGLSKQIOIASTNNGQFSPVLLINAQORVTITNVDAVGTSTNIAL 263  
Db 204 PSIAITISLENSWGLSKQIOIASTNNGQFSPVLLINAQORVTITNVDAVGTSTNIAL 263

QY 241 LNENMMA 247  
Db 241 LNENMMA 247

RESULT 6

S22494  
rRNA N-glycosidase (EC 3.2.2.22) alpha-luffin precursor - smooth loofah  
N/Alternate names: protein synthetase inhibitor; ribosome-inactivating protein luffin-A  
C/Species: Luffa cylindrica (smooth loofah)  
C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
C/Accession: S22494; S26390; JH0202; A32542  
R/Kataoka, J.; Habuka, N.; Miyano, M.; Masuda, C.; Koiwai, A.  
Plant Mol. Biol. 18, 1199-1202, 1992  
A/Title: Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-inactivating pro  
A/Reference number: S22494; PMID:92288316; PMID:1600156  
A/Accession: S22494

A:Molecule type: mRNA  
A:Residues: 1-277 <KAT>  
A:Cross-references: UNIPROT:Q00465; EMBL:X62371; NID:g19145; PIDN:CAA44229.1; PID:g19146  
R:Islam, M.R.; Nishida, H.; Funatsu, G.  
Agric. Biol. Chem. 54, 2967-2978, 1990  
A:title: Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from  
A:Reference number: S26390; MWID:91248471; PMID:1368651  
A:Accession: S26390  
A:Molecule type: protein  
A:Residues: 21-53, 'L', '55', 'I', '57-86', 'SQL', '90-154', 'L', '156-157', 'I', '159-173', 'L', '175-209', 'SL'  
R:Islam, M.R.; Nishida, H.; Funatsu, G.  
Agric. Biol. Chem. 54, 1343-1345, 1990  
A:title: Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from  
A:Reference number: JH0202; MWID:91197482; PMID:1368623  
A:Accession: JH0202  
A:Molecule type: protein  
A:Residues: 21-53, 'L', '55', 'I', '57-86', 'SQL', '90-154', 'L', '156-157', 'I', '159-173', 'L', '175-209', 'SL'  
A:Experimental source: Seed  
R:Ramakrishnan, S.; Englund, J.J.; Bryant Jr., H.L.; Xu, F.J.  
Biochem. Biophys. Res. Commun. 160, 509-516, 1989  
A:title: Characterization of a translation inhibitory protein from luffa aegyptiaca.  
A:Reference number: A32542; MWID:89246493; PMID:2719679  
A:Accession: A32542  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 21-28, 'G', '30', 'X', '32-34', 'K', '36-40 <RAM>  
C:Function:  
A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA then  
C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
C:Keywords: glycoprotein, glycosidase, hydrolase, seed, toxin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-267/Domain: signal sequence #status predicted <SIG>  
F:24-262/Domain: RNA N-glycosidase alpha-luffin #status experimental <MAT>  
F:268-277/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F:148,53,97,104,225,246/Binding site: carbohydrate (Aen) (covalent) #status experimental  
F:90,179,182/Active site: Tyr, Glu, Arg #status predicted

Query Match 61.8%; Score 754; DB 2; Length 277;  
Best Local Similarity 62.1%; Pred. No. 6.3e-56;  
Matches 154; Conservative 42; Mismatches 50; Indels 2; Gaps 2;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLDIPILRSSLPQSQRVALIHLTNVADETI 60  
DB 21 DVFRLSSGSSSTYSRFDLDRKALPSNGRYITLLSSASGASRYITLMTLSNYYGKAI 80  
QY 61 SVAIDVTNYIMGYRAGDTSYFNEASATEAKYVFKAMRKVTLPSYGNVERLQTAAGK 120  
DB 81 TVAVDVTNYIMGYLVNSTSYFNEBDAKLASQYFKGS-TIVTLPSYGNVERLQTAAGK 139  
QY 121 IRENIPILGIPALDSAITTLFYNNANSASALMWLIQSTSEARVYKFEIQIGKRVDTFL 180  
DB 140 IREKIPILGIPALDSAITTLFHYDSTAAAFVLIQTTEASRFXIEQIIERIKNOY 199  
QY 181 PSLAIIISLNSWSALSKQIQIASTNNGQFESPVVLINQONRVTTNVDAVTSNIAL 240  
DB 200 PSLAIIISLNSWSALSKQIQIASTNNGQFESPVVLINQONRVTTNVDAVTSNIAL 259  
QY 241 LN-RNNMA 247  
DB 260 LNKQNIYA 267

RESULT 7  
S23519  
beta-luffin - smooth loofah  
C:Species: luffa cylindrica (smooth loofah)  
C:date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C:Accession: S23519; S23113  
R:Katoka, T.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.  
Plant Mol. Biol. 19, 887-889, 1992  
A:title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivating  
A:Reference number: S23519; MWID:92353400; PMID:1643290  
A:Accession: S23519

A:Molecule type: mRNA  
A:Residues: 1-278 <KAT>  
A:Cross-references: UNIPROT:Q00980; EMBL:X62372; NID:g19149; PIDN:CAA44230.1; PID:g19150  
C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
F:26-264/Domain: RNA N-glycosidase homology <RNG>

Query Match 59.7%; Score 728.5; DB 2; Length 278;  
Best Local Similarity 59.9%; Pred. No. 8.9e-54;  
Matches 148; Conservative 44; Mismatches 54; Indels 1; Gaps 1;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLDIPILRSSLPQSQRVALIHLTNVADETI 60  
DB 23 NVSFSLSGADSKSYKFTALRKALPSKESNIPLLPLPSASGASRYITLMQISNDAKAI 82  
QY 61 SVAIDVTNYIMGYRAGDTSYFNEASATEAKYVFKAMRKVTLPSYGNVERLQTAAGK 120  
DB 83 TVAIDVTNYIMGYLVNSTSYFNEBDAKLASQYFKGS-TIVTLPSYGNVERLQTAAGK 141  
QY 121 IRENIPILGIPALDSAITTLFYNNANSASALMWLIQSTSEARVYKFEIQIGKRVDTFL 180  
DB 142 VREKIPILGIPALDSAITTLFHYDSTAAAFVLIQTTEASRFXIEQIIERIKNEV 201  
QY 181 PSLAIIISLNSWSALSKQIQIASTNNGQFESPVVLINQONRVTTNVDAVTSNIAL 240  
DB 202 PSLAIIISLNSWSALSKQIQIASTNNGQFESPVVLINQONRVTTNVDAVTSNIAL 261  
QY 241 LN-RNNMA 247  
DB 262 LNKQNIYA 268

RESULT 8  
S25560  
RNA N-glycosidase (BC 3.2.2.22) momordin II - balsam apple  
C:Species: Momordica balsamina (balsam apple)  
C:date: 25-Feb-1994 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: S25560  
R:Ortigao, M.; Better, M.  
Nucleic Acids Res. 20, 4662, 1992  
A:title: Momordin II, a ribosome inactivating protein from Momordica balsamina, is homol  
A:Reference number: S25560; MWID:93027170; PMID:1408771  
A:Accession: S25560  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Cross-references: UNIPROT:P29339; EMBL:212175; NID:g19525; PIDN:CAA78166.1; PID:g19526  
C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
C:Keywords: glycosidase, hydrolase  
F:27-264/Domain: RNA N-glycosidase homology <RNG>

Query Match 58.1%; Score 709; DB 2; Length 286;  
Best Local Similarity 61.6%; Pred. No. 4e-52;  
Matches 149; Conservative 30; Mismatches 61; Indels 2; Gaps 2;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLDIPILRSSLPQSQRVALIHLTNVADETI 60  
DB 24 DVNFDLSTATKTYTKFIEDFRATLPFSHKVYDIPILVSTISDSRFLDLTSYAVETI 83  
QY 61 SVAIDVTNYIMGYRAGDTSYFNEASATEAKYVFKAMRKVTLPSYGNVERLQTAAGK 120  
DB 84 SVAIDVTNYVAVYRTRVVSYPFKE-SPEEANNILF-GTRKITLPYGNENMTQTAARK 141  
QY 121 IRENIPILGIPALDSAITTLFYNNANSASALMWLIQSTSEARVYKFEIQIGKRVDTFL 180  
DB 142 IRENIDLGIPALDSAITTLFYNNASASALMWLIQTTAEARFXIERHAKVATNFK 201  
QY 181 PSLAIIISLNSWSALSKQIQIASTNNGQFESPVVLINQONRVTTNVDAVTSNIAL 240  
DB 202 PSLAIIISLNSWSALSKQIQIASTNNGQFESPVVLINQONRVTTNVDAVTSNIAL 261  
QY 241 LN 242  
DB 262 LN 263



## RESULT 9

JC4235

rRNA N-glycosidase (EC 3.2.2.22) map30 precursor - balsam pear

N/Alternate names: anti-HIV 30K protein

C/Species: Momordica charantia (balsam pear, bitter melon)

C/Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004

C/Accession: J04235, S12869

R/Ref: Huang, S.; Huang, P.L.; Chen, H.C.; Huang, P.L.; Bourinbatar, A.; Huang, H.I.; Kuo

Gene 161, 151-156, 1995

A/Title: Anti-HIV and anti-tumor activities of recombinant MAP30 from bitter melon.

A/Reference number: J04235; MUID:95394347; PMID:7665070

A/Accession: J04235

A/Molecule type: DNA

A/Residues: 1-286 &lt;LSE&gt;

A/Cross-references: UNIPROT:P24817

A/Experimental source: mature seeds

A/Note: The authors translated the codon TAC for residue 37 as Thr and ACT for residue 1

R/Ref: Huang, S.; Huang, P.L.; Nara, P.L.; Chen, H.C.; Kung, H.; Huang, P.; Huang, H.I.;

FEBS Lett. 272, 12-18, 1990

A/Title: MAP 30: a new inhibitor of HIV-1 infection and replication.

A/Reference number: S12869; MUID:91032105; PMID:1699801

A/Accession: S12869

A/Molecule type: protein

A/Residues: 24-36, 'r', '38-66, 'p' &lt;LSE&gt;

C/Comment: This plant protein has anti-HIV activity. It possesses antiviral action, anti

activation activities. It is capable of acting against multiple stages of the viral life

C/Comment: This protein has conserved unique residues Trp-213 and Met-277.

C/Genetics:

A/Genes: map30

C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C/Keywords: antiviral; glycoprotein; glycosidase; hydrolase

F/1-23/Domain: signal sequence #status predicted &lt;SIG&gt;

F/24-286/Product: rRNA N-glycosidase (EC 3.2.2.22) map30 #status predicted &lt;MAT&gt;

F/27-264/Domain: rRNA N-glycosidase homology &lt;RNG&gt;

F/4/Binding site: carbohydrate (Asn) (covalent) #status predicted

F/33,181,184/Active site: Tyr, Glu, Arg #status predicted

Query Match

Best Local Similarity 57.8%; Score 706; DB 2; Length 286;

Matches 148; Conservative 31; Mismatches 61; Indels 2; Gaps 2;

QY 1 DVSFRLSGATSSGYGFISNLKRALPNEKLYDIPILRSLSGSRVALIHLTNVDEIT 60

DB 24 DVNFDISTATKYTFIEBFRATLPFSHKYDIPILYSTRISDRFFILNLTYSAYEIT 83

QY 61 SVAIDVTNYIMGYRAGDTSYFNEASATEAKYVFDAMRKVTLPSGNYERLQTAAGK 120

DB 84 SVAIDVTNYVAVYKRDVSYPFKE-SPPAVNYILFK-GTRKTLTPYGVENLQTAHAK 141

QY 121 IRENIPGLPALDSATITLTFYNNASASALMWLIQSTSEARVKFIEQIGKRVDTFL 180

DB 142 IRENIDGLPALDSATITLTFYNNASASALMWLIQSTSEARVKFIEQIGKRVDTFL 201

QY 181 PSIAITISLSEWSALSQIOIASTNNGQFESPVLINAOQRTITNVDAVTSNIAL 240

DB 202 PNIAITISLSEWSALSQIOIASTNNGQFESPVLINAOQRTITNVDAVTSNIAL 261

QY 241 LN 242

DB 262 LN 263

## RESULT 10

JN0108

luffin-b - smooth loofah

C/Species: luffa cylindrica (smooth loofah)

C/Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 09-Jul-2004

C/Accession: JN0108

R/Ref: Islam, M.R.; Htayama, H.; Funatsu, G.

Agric. Biol. Chem. 55, 229-238, 1991

A/Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from

A/Reference number: JN0108; MUID:91248488; PMID:1368666

A/Accession: JN0108

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-250 &lt;ISL&gt;

A/Cross-references: UNIPROT:P22851

C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

F/5-246/Domain: rRNA N-glycosidase homology &lt;RNG&gt;

Query Match

Best Local Similarity 55.7%; Score 680; DB 2; Length 250;

Matches 142; Conservative 47; Mismatches 57; Indels 4; Gaps 3;

QY 1 DVSFRLSGATSSGYGFISNLKRALPNEKLYDIPILRSLSGSRVALIHLTNVDEIT 60

DB 2 NVFSLSGADSKSYKFTALRKALPSKERVNIPLLPSASGASRYTLMQSLNDAKAI 61

QY 61 SVAIDVTNYIMGYRAGDTSYFNEASATEAKYVFDAMRKVTLPSGNYERLQTAAGK 120

DB 62 TMAIDVTNYIMGYLVNSTYFANESDALKASQYFPGS-TLVITYSGNYERLQTAAGK 120

QY 121 IRENIPGLPALDSATITLTFYNNASASALMWLIQSTSEARVKFIEQIGKRVDTFL 180

DB 121 IREKIPGLPALDSATITLTFYNNASASALMWLIQSTSEARVKFIEQIGKRVDTFL 180

QY 181 PSIAITISLSEWSALSQIOIASTNNGQFESPVLINAOQRTITNVDAVTS--NI 237

DB 181 PSIAITISLSEWSALSQIOIASTNNGQFESPVLINAOQRTITNVDAVTS--NI 237

QY 238 ALLINNNMNA 247

DB 241 KLLNNKONIA 250

## RESULT 11

JC4840

rRNA N-glycosidase (EC 3.2.2.22) trichoanguina - snake gourd

C/Species: Trichosanthes anguina (snake gourd)

C/Date: 15-Aug-1996 #sequence\_revision 24-Oct-1997 #text\_change 05-Dec-1997

C/Accession: JC4840; J070701; J0677

R/Chow, L.P.; Kamo, M.; Lin, J.Y.; Wang, S.H.; Ueno, Y.; Tsugita, A.

Biomed. Sci. 3, 178-186, 1996

A/Title: Amino acid of sequence of trichoanguina, a ribosomal-inactivating protein from

A/Reference number: JC4840

A/Accession: JC4840

A/Molecule type: protein

A/Residues: 1-132, 'S', 134-245 &lt;CHO1&gt;

A/Experimental source: seed

A/Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Table

R/Chow, L.P.; Kamo, M.; Lin, J.Y.; Ueno, Y.; Tsugita, A.

submitted to JIPID, August 1995

A/Description: Amino acid sequence of trichoanguina, a ribosomal-inactivating protein from

A/Reference number: J0677

A/Accession: J070701

A/Molecule type: protein

A/Residues: 1-50, 'L', 52-245 &lt;CHO2&gt;

C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C/Keywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed

F/4-242/Domain: rRNA N-glycosidase homology &lt;RNG&gt;

F/51,201/Binding site: carbohydrate (Asn) (covalent) #status experimental

F/70,158,161/Active site: Tyr, Glu, Arg #status predicted

F/155/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match

Best Local Similarity 54.6%; Score 666.5; DB 2; Length 245;

Matches 138; Conservative 34; Mismatches 67; Indels 3; Gaps 3;

QY 1 DVSFRLSGATSSGYGFISNLKRALPNEKLYDIPILRSLSGSRVALIHLTNVDEIT 60

DB 1 DVNFDISTATKYTFIEBFRATLPFSHKYDIPILYSTRISDRFFILNLTYSAYEIT 83

QY 61 SVAIDVTNYIMGYRAGDTSYFNEASATEAKYVFDAMRKVTLPSGNYERLQTAAGK 120

DB 241 KLLNNKONIA 250

Db 61 TVADVNNVYIVAIRADAVSYFFEDTPA-EAFKLIFA-GTKTVKLPYSGNTDKLOSVMGK 118

QY 121 IRENIPIGLPALDSAITTLFYNNANSAASALMWLIQSTSEARVYKFEIOQIGRVDTFL 180

Db 119 QRDMIELGIPALSSAITNMWYYDYQSTAAALLVLQSTAEARVYKIEQOYSSHTSSNFY 178

QY 181 PSLAIISLENSWSALSKOIQIAS-TNNGOFESPVLINAQORVTTINVDAGVYTSNIAL 239

Db 179 PNOAVISLENNKMGALSIOQIANRFGHGQFENFELVNPDCGRFREVTHTSAGVYGNIKL 238

QY 240 LL 241

Db 239 LL 240

## RESULT 12

Ricin D precursor - castor bean

N:Contains: rRNA N-glycosylase (EC 3.2.2.22)

C:Species: Ricinus communis (castor bean)

C:Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903

C:Update: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 09-Jul-2004

A:Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene

A:Reference number: S20513; PMID:92163016; PMID:1371405

A:Accession: A24041

A:Molecule type: DNA

A:Residues: 1-576 <HML>

A:Cross-references: UNIPROT:P02879; GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083

R:Tregear, J.W.; Roberts, L.M.

Plant Mol. Biol. 18, 515-525, 1992

A:Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene

A:Reference number: S20513; PMID:92163016; PMID:1371405

A:Accession: A24041

A:Molecule type: DNA

A:Residues: 1-576 <TRE>

A:Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085

R:Lamb, F.I.; Roberts, L.M.; Lord, J.M.

Eur. J. Biochem. 148, 265-270, 1985

A:Title: Nucleotide sequence of cloned cDNA coding for preproricin.

A:Reference number: A24614; PMID:85179479; PMID:3838723

A:Accession: A24614

A:Molecule type: mRNA

A:Residues: 12-75; 'D', 77-550, 'R', 552-576 <LAM>

A:Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078

R:Yoshitake, S.; Funatsu, G.; Funatsu, M.

Agaric. Biol. Chem. 42, 1267-1274, 1978

A:Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile ch

A:Reference number: A03372

A:Accession: A03372

A:Molecule type: Protein

A:Residues: 36-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'I', 285-288, 290-302 <YOS>

A:Note: This paper cites the others in the series providing experimental details for the

R:Araaki, T.; Funatsu, G.

FEBS Lett. 191, 121-124, 1985

A:Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A:Reference number: A24010

A:Accession: A24010

A:Molecule type: Protein

A:Residues: 315-383, 'PS', 386-576 <ARA>

R:Funatsu, G.; Kimura, M.; Funatsu, M.

Agaric. Biol. Chem. 43, 2221-2224, 1979

A:Title: Primary structure of Ala chain of ricin D.

A:Reference number: A03374

A:Accession: A03374

A:Molecule type: Protein

A:Residues: 315-335, 'N', 337-342, 'NH', 345-362, 364-383, 'RS', 386-399, 'T', 401, 'D', 403, 'E', 403, 'E', 529-564, 'W', 566, 'H', 567-570, 'LI', 573-574, 'F' <FUN>

A:Note: This paper, one of a series, summarizes the experimental details for the determin

R:Ready, M.P.; Kim, Y.; Robertus, J.D.

Proteins 10, 270-278, 1991

A:Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism c

A:Reference number: A48237; MUID:91352006; PMID:181863  
A:Contents: annotation; active site  
R:Rutember, E.; Robertus, J.D.  
P:protein 10, 260-269, 1991  
A:Title: Structure of ricin B-chain at 2.5 angstrom resolution.  
A:Reference number: A48238; MUID:91352005; PMID:181862  
A:Contents: annotation; X-ray crystallography, 2.5 angstroms  
R:Katzin, B.J.; Collins, E.J.; Robertus, J.D.  
P:protein 10, 251-259, 1991  
A:Title: Structure of ricin A-chain at 2.5 angstroms.  
A:Reference number: A48239; MUID:91352004; PMID:181861  
A:Contents: annotation; X-ray crystallography, 2.5 angstroms  
C:Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which  
C:Comment: The A chain inhibits protein synthesis; it inactivates the 60S ribosomal subu  
nto the cell of the A chain. B chains are also responsible for cell agglutination (lecti  
C:Comment: This protein is cytotoxic and very poisonous to animals.  
C:Superfamily: ricin; rRNA-N-glycosidase homology  
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed  
F:1-35/Domain: signal sequence #status predicted <Sig>  
F:36-302/Product: ricin D chain A #status predicted <ACH>  
F:46-293/Domain: rRNA-N-glycosidase homology <NG>  
F:515-576/Product: ricin D chain B #status experimental <BC>  
F:531-373;574-414;417-455;462-497;501-540;543-576/Region: 40-residue repeats  
F:445;409;449/binding site: carboxylate (Asn) (covalent) #status experimental  
F:115;158;243;244/binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F:212/Active site: Glu #status experimental  
F:215/Active site: Arg #status predicted  
F:299-318;334-353;377-394;465-478;504-521/disulfide bonds: #status experimental  
F:336;349;360/binding site: N-acetylglucosamine (Asp, Glu, Asn) #status experimental  
F:548;569/binding site: N-acetylglucosamine (Asp, Asn) #status experimental

Query Match

Query Match	34.5%;	Score 421;	DB 1;	Length 576;
Best Local Similarity	37.3%;	Pred. No. 1.7e-27;		
Matches	95;	Conservative	60;	Mismatches 82;
			Indels	18;
			Gaps	8

[illegible]

## RESULT 13

RLCSAG

agglutinin precursor - castor bean  
N/Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C/Species: Ricinus communis (castor bean)  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #ext\_change 09-Jul-2004  
C/Accession: A24261; A24210  
R/Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.  
J. Biol. Chem. 260, 15682-15686, 1985  
A/Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.  
A/Reference number: A24261; M0ID:86059449; PMID:299130  
A/Accession: A24261  
A/Molecule type: mRNA  
A/Residues: 1-564 <ROB>  
A/Cross-references: UNIPROT:P06750; GB:M12089; NID:G169700; PIRN:AAA33869.1; PID:G169701  
R/Araki, T.; Yoshioaka, Y.; Funatsu, G.  
Biochim. Biophys. Acta 872, 277-285, 1986

A>Title: The complete amino acid sequence of the B-chain of the *Rhizinus communis* agglutinin  
A:Reference number: A24210  
A:Accession: A24210  
A:Molecule type: Protein  
A:Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-564  
C:Comment: This protein has strong agglutinating activity and weak cytotoxicity compared to other ricin agglutinins.  
C:Superfamily: ricin; rRNA N-glycosidase homology  
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed  
F:1-24/Domains: signal sequence #status predicted <SIG>  
F:25-290/Product: agglutinin chain A #status predicted <ACH>  
F:35-281/Domains: rRNA N-glycosidase homology <RNG>  
F:303-564/Product: agglutinin chain B #status experimental <BCH>  
F:319-351, 362-402, 405-443, 450-485, 489-528, 531-554/Region: 40-residue repeats  
F:334,259/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F:100,203/Active site: Glu, Arg #status predicted  
F:128-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted  
F:323,327,348/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status predicted  
F:329,337/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:356,557/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match	32.5%	Score 396.5;	DB 1;	Length 564;
Best Local Similarity	37.3%	Pred. No. 1.9e-25;		
Matches 95; Conservative	55;	Mismatches 86;	Indels 19;	Gaps 9;

QY 2 V\$FRL\$GAT\$SS\$YGV\$FINL\$RKAL\$EN\$RKL--VDI\$PL--R\$SL\$P\$G\$Q\$Y\$A\$IL\$H\$TN\$Y\$D\$E 58

Db 33 INFT\$AD\$TV\$ES\$Y\$TN\$F\$IR\$AV\$SH\$L\$TG\$AD\$V\$H\$E\$IV\$L\$EN\$R\$V\$EL\$P\$IS\$Q\$F\$IL\$E\$V\$LS\$NH\$A\$EL 92

QY 59 TIS\$VA\$ID\$VT\$NY\$IM\$G\$Y\$R\$AG\$DT\$SY\$F--NE\$AS\$AT\$A\$K\$Y\$F\$D\$A\$R\$K\$Y\$L\$P\$Y\$G\$N\$Y\$ER\$L\$Q 115

Db 93 SVT\$L\$AD\$VT\$NN\$Y\$V\$G\$C\$R\$A\$G\$N\$S\$A\$Y\$F\$P\$H\$D\$O\$E\$D\$A--E\$A\$IH\$L\$FT\$D\$V\$G\$N\$S\$T\$F\$P\$A\$G\$G\$Y\$D\$R\$L\$E 151

QY 116 T\$A\$G\$K\$IR\$E\$N\$IP\$L\$G\$AL\$D\$AL\$S\$A\$IT\$L\$E\$Y\$Y\$N\$A-----N\$S\$A\$S\$AL\$M\$V\$L\$Q\$S\$E\$A\$R\$Y\$E\$F\$E\$EQ 170

Db 152 Q\$U\$G--L\$R\$E\$N\$IE\$IG\$T\$P\$L\$E\$D\$A\$IS\$AL\$Y\$Y\$T\$C\$G\$T\$Q\$IT\$L\$R\$S\$F\$W\$V\$C\$I\$O\$M\$I\$S\$E\$A\$R\$F\$O\$Y\$E\$GE 210

QY 171 I\$G\$R\$V--D\$K\$T\$P\$L\$S\$A\$I\$IS\$L\$E\$N\$S\$W\$S\$AL\$S\$K\$O\$I\$D\$A\$S\$T\$N\$G\$E\$S\$P\$V\$L\$I\$N\$A\$Q\$N\$O\$R\$T\$I\$N\$V 228

Db 211 M\$R\$T\$R\$A\$Y\$R\$R\$S\$A\$P\$D\$P\$S\$V\$IT\$L\$E\$N\$S\$W\$O\$R\$L\$S\$T\$A\$ID--E\$S\$N\$G\$A\$F\$A\$S\$P\$Q\$L\$O\$R\$R\$G\$S\$K\$E\$N\$V--Y 266

QY 229 D\$A\$G\$V\$T\$S\$N\$A\$IL\$A\$IL\$N\$R 243

Db 267 D\$V\$S\$I\$L\$IP\$T\$A\$LM\$Y\$R 281

RESULT 14  
C39761

A:brin (clone 7.2) precursor - Indian licorice (fragment)  
 N:Contains: rRNA N-glycosidase (EC 3.2.2.22)  
 C:Species: *Abrus precatorius* (Indian licorice)  
 C:date: 21-Feb-1992 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C:Accession: C39761; S14471  
 R:Evensen, G.; Machielsen, A.; Sundan, A.  
 J. Biol. Chem. 266, 6848-6852, 1991  
 A:title: Direct molecular cloning and expression of two distinct abrin A-chains  
 A:Reference number: A39761; MUID:91201329; PMID:2016300  
 A:Accession: C39761  
 A:Molecule type: DNA  
 A:Residues: 1-251 <EVE>  
 A:Cross-references: UNIPROT:Q38760  
 R:Evensen, G.; Machielsen, A.; Sundan, A.  
 submitted to the EMBL Data Library, October 1990  
 A:description: Direct molecular cloning of two distinct abrin A-chains.  
 A:Reference number: S14471  
 A:Accession: S14471  
 A:Molecule type: DNA  
 A:Residues: 'W', 1-251 <EVE>  
 A:Cross-references: EMBL:X54872; NID:G16088; PIDN:CAA8654.1; PID:G16089  
 C:Superfamily: ricin; rRNA N-glycosidase homology  
 C:Keywords: duplication; glycosidase; hydrolyase; lectin; toxin  
 P:1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>  
 F:7-246/Domain: rRNA N-glycosidase homology <RMS>

F:74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F:164,167/Active site: Glu, Arg #status predicted

Query Match	28.8%	Score 352	DB 2	Length 251
Best Local Similarity	38.6%	Pred. No. 3.4e-22		
Matches 95	Conservative 42	Mismatches 97	Indels 12	Gaps 8

0y 2 VSRRLSGATSSSTGVFIINLRKLPNERKLVDIPLLR--SSLEQSORALIHITVYADET 59  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 5 IKRTGEGTSQSKOIFIALREL-RGLIHIDIPVKRPDPTVEERNRIITVELSNSEKES 63

Oy 60 ISVAIDPNNVIMGYRAGDTSPEFNESASATEAKVFEDAMRKTLPVSGNIYERLOTPAAG 119  
| | | | : | : | : | :  
Db 64 IEKGIDTNAVAVAYRAGSQSFILRDAPASASTYLPLFGTORYSLRDGSTGDLERWAH 121

---

87

QY 120 KTRRNNPLGLPALDSATFTL--FYNNNSAASALMTVIQSTEEAARXYEEIQQG--RV 175  
 122 QTRRQISGLQALTHAISFLRGSANDBEKARLIVITQMASEAARRYITSNRVGVSIRT 181  
 Db

Qy 176DKFELPSLAIISLPSNMGALSXQIQIAIQTSTNNQGFESPVLINLQNRQITITNDVAGVYTS 235  
::: :::: :  
Db 182GTAFQPDPAMLSTLNNMDNLKRVQ--ESVDTFPNAVTLRRVNNQPIVDSLTHTQSY-A 238

Qy	236	NIALML	241
	:	:	:
	:	:	:
Db	239	VIALML	244

RESULT 15  
822431

N-Contains: rRNA N-glycosylase (EC 3.2.2.22)  
C.Species: *Abrus precatorius* (Indian licorice)  
C.Date: 30-Sep-1993 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004

**Authors:** R. Hung, C.H. Lee, M.C. Lee, T.C. Lin, J.Y. J. Mol. Biol. 225, 263-267, 1993

**Article:** Primary structure of three distinct isobornins determined by cDNA sequence

A:Accession: S32431  
A:Molecule type: mRNA  
A:Residues: 1-528 <HUN>

R.Hung, C.i.lee, M.i.lee, T.i.lin, J.  
submitted to the EMBL Data Library, March 1993  
A.Reference number: S34408

A: Molecule type: mRNA  
A: Residues: 1-169, 'C', 171-320, 'L', 322-528 <HU2>  
A: Cross-references: GB:M9346

**Abstract:** The A and B chains are linked by a single disulfide bond, which is essential for the function of the enzyme. The A chain contains a single cysteine residue, which is essential for the function of the enzyme. The B chain contains a single cysteine residue, which is essential for the function of the enzyme. The A and B chains are linked by a single disulfide bond, which is essential for the function of the enzyme. The A chain contains a single cysteine residue, which is essential for the function of the enzyme. The B chain contains a single cysteine residue, which is essential for the function of the enzyme.

F: 7-2246/Domain: rRNA N-glycosidase homology <RNG>  
E: 261-528/Product: abrin-d chain B #status predicted <BCG>  
F: 283-325, 326-366, 369-407, 414-449, 453-492, 495-528/Region: 40-residue repeats

F:74.113,193/96/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F:164,167/active site: Glu, Arg #status predicted  
F:200,253,351,401,402/Binding site: carbohydrate (Asn) (covalent) #status predi  
F:200,253,351,401,402/Binding site: carbohydrate (Asn) (covalent) #status predi

Accession Number	Gene	DB	Month	Year
F_288_312/Banding site:	N-acetylglactosamine (Asp, Asn)	#status predicted		
F_500_521/Banding site:	N-acetylglactosamine (Asp, Asn)	#status predicted		

On 2 VAFPI,SCATSSSCVCTCSTNTPKYIPNRPKTYNTPII,--PSSY,PGSCQVAT,IRH,TNVADET 59  
Matches 93; Conservativity 43; Mismatches 98; Indels 12; Gaps 8;

Db 5 IKETEGATSGSQKQFIETALRQLTG-GLIHIDIPVLEPDTVEERNRRIYVELSNSERES 63

QY 60 ISVAIDVTNYINGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPGSGNYERLQTAAG 119  
Db 64 IEVGIDVTNAYVAYRAGSQSYFLRDPAS-ASTYLFPGTOR-YSLRFDGSYGDLERWLH 121  
QY 120 KIRENIPLGHPALDSAITTL--FYVANSASALMTLIQSTSEARYPFIEQIGK--RV 175  
Db 122 QFREESISLGQALTTAHSFLRSGASNDEEKARTLIVIQMASEARRYISNRVGSIRT 181  
QY 176 DKTFPLSLAIIISLNSMSALSQIOIASTNNQFESPVVLIINAQONRVITITNVDAGVTS 235  
Db 182 GTRFQDPDPMLSLENNWNLSSGVQ--QSVQDTFPNNVILSSINRQPVVDSLSHPTV-A 238  
QY 236 NIALLL 241  
Db 239 VLALML 244

Search completed: April 12, 2005, 15:14:59  
Job time : 26.3451 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 12, 2005, 15:14:19 ; Search time 81.5653 Seconds  
(without alignments)  
1005.370 Million cell updates/sec

Title: US-09-905-247a-8  
Perfect score: 1221  
Sequence: 1 DVAFRLSGATSSSYGVFISN.....VDAGVVTSNALLLNRRNNA 247

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues  
Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubppa/PTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1221	100.0	247	9 US-09-792-793A-39	Sequence 39, Appl
2	1221	100.0	247	15 US-10-375-209A-39	Sequence 39, Appl
3	1214	99.4	288	11 US-09-905-247-1	Sequence 1, Appl
4	1212	99.3	289	14 US-10-280-679B-4	Sequence 4, Appl
5	1212	99.3	289	15 US-10-280-725B-4	Sequence 4, Appl
6	1209	99.0	247	14 US-10-127-890-6	Sequence 6, Appl
7	1209	99.0	247	17 US-10-717-243-6	Sequence 6, Appl
8	1071	87.7	247	9 US-09-792-793A-34	Sequence 34, Appl
9	1071	87.7	247	15 US-10-375-209A-34	Sequence 34, Appl
10	802	65.7	263	14 US-10-127-890-7	Sequence 7, Appl
11	802	65.7	263	17 US-10-717-243-7	Sequence 7, Appl
12	724.5	59.3	248	14 US-10-127-890-5	Sequence 5, Appl
13	724.5	59.3	248	17 US-10-717-243-5	Sequence 5, Appl

14	709	58.1	263	14	US-10-127-890-4	Sequence 4, Appl
15	709	58.1	263	17	US-10-717-243-4	Sequence 4, Appl
16	421	34.5	267	14	US-10-282-935-1	Sequence 1, Appl
17	421	34.5	267	14	US-10-127-890-1	Sequence 1, Appl
18	421	34.5	267	15	US-10-440-796-1	Sequence 1, Appl
19	421	34.5	267	17	US-10-717-243-1	Sequence 1, Appl
20	421	34.5	267	14	US-10-083-336A-1	Sequence 1, Appl
21	342	28.0	198	14	US-10-083-336A-1	Sequence 3, Appl
22	342	28.0	198	14	US-10-083-336A-7	Sequence 3, Appl
23	342	28.0	198	14	US-10-083-336A-5	Sequence 5, Appl
24	342	28.0	198	14	US-10-083-336A-10	Sequence 10, Appl
25	337.5	27.6	185	14	US-10-083-336A-9	Sequence 9, Appl
26	336	27.5	188	14	US-10-083-336A-4	Sequence 4, Appl
27	336	27.5	188	14	US-10-083-336A-8	Sequence 8, Appl
28	336	27.5	189	14	US-10-083-336A-6	Sequence 6, Appl
29	336	27.5	190	14	US-10-083-336A-11	Sequence 11, Appl
30	330	27.0	251	14	US-10-282-935-3	Sequence 3, Appl
31	330	27.0	251	15	US-10-440-796-3	Sequence 2, Appl
32	326	26.7	252	9	US-09-347-064-2	Sequence 8, Appl
33	326	26.7	252	14	US-10-127-890-9	Sequence 9, Appl
34	323	26.5	251	14	US-10-127-890-101	Sequence 101, App
35	323	26.5	251	14	US-10-127-890-107	Sequence 107, App
36	323	26.5	251	17	US-10-717-243-99	Sequence 99, Appl
37	323	26.5	251	17	US-10-717-243-101	Sequence 101, App
38	323	26.5	251	17	US-10-717-243-107	Sequence 107, App
39	322	26.4	251	14	US-10-127-890-110	Sequence 110, App
40	322	26.4	251	14	US-10-127-890-111	Sequence 111, App
41	322	26.4	251	17	US-10-717-243-110	Sequence 110, App
42	322	26.4	251	17	US-10-717-243-111	Sequence 111, App
43	322	26.4	251	9	US-09-765-527-247	Sequence 247, App
44	321	26.3	251	14	US-10-127-890-2	Sequence 2, Appl
45	321	26.3	251	14	US-10-127-890-2	Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-09-792-793A-39  
Sequence 39, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 39  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Trichosantheus kirilowii  
US-09-792-793A-39

Query Match 100.0%; Score 1221; DB 9; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.7e-112;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DVAFRLSGATSSSYGVFISNLRKALNERKLYDIPILRSGLPSQRYALHLTNVADDTT 60
DB	1	DVAFRLSGATSSSYGVFISNLRKALNERKLYDIPILRSGLPSQRYALHLTNVADDTT 60
QY	61	SVADIDVTNYIMGYRAGDTSYFENEASATEAKYVKDMARKYTLFYSQGYEYLQTAAGK 120
DB	61	SVADIDVTNYIMGYRAGDTSYFENEASATEAKYVKDMARKYTLFYSQGYEYLQTAAGK 120
QY	121	IRENIFLGLPALDSAITTLFYYNANSASALMWLIQSTSEARAKYFEOQIGKRVKXFL 180
DB	121	IRENIFLGLPALDSAITTLFYYNANSASALMWLIQSTSEARAKYFEOQIGKRVKXFL 180

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QY      181  PSIAIISLNSWSALS KQIQIASTNNQGFESPVLINQNRVTITNVDAVGTSTNIALL 240
      |||||||
DB      181  PSIAIISLNSWSALS KQIQIASTNNQGFESPVLINQNRVTITNVDAVGTSTNIALL 240

QY      241  LNRNNMA 247
      |||||||
DB      241  LNRNNMA 247

RESULT 2
US-10-375-209A-39
; Sequence 39, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Cogdins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; FILE REFERENCE: 25020-601E
; CURRENT APPLICATION NUMBER: US/10/375,209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Trichosanthes kirilowii
US-10-375-209A-39

Query Match      100.0%; Score 1221; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.7e-112;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 60
      |||||||
DB      1  DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 60

QY      61  SVAIDVTNYYIMGYRAGDTSYFFENASATEAKYVFKDAMRKVTLPYSGNVERLQTAAGK 120
      |||||||
DB      61  SVAIDVTNYYIMGYRAGDTSYFFENASATEAKYVFKDAMRKVTLPYSGNVERLQTAAGK 120

QY      121  IRENIPGLGIPALDSAITTLFPYNNASASALMWLIQSTSEARRYFIEQIQKRVDTFTL 180
      |||||||
DB      121  IRENIPGLGIPALDSAITTLFPYNNASASALMWLIQSTSEARRYFIEQIQKRVDTFTL 180

QY      181  PSIAIISLNSWSALS KQIQIASTNNQGFESPVLINQNRVTITNVDAVGTSTNIALL 240
      |||||||
DB      181  PSIAIISLNSWSALS KQIQIASTNNQGFESPVLINQNRVTITNVDAVGTSTNIALL 240

QY      241  LNRNNMA 247
      |||||||
DB      241  LNRNNMA 247

RESULT 3
US-09-905-247-1
; Sequence 1, Application US/09905247
; Publication No. US20040197853A1
; GENERAL INFORMATION:
; APPLICANT: KE, YI-BAO
; APPLICANT: NIE, HUI-LING
; TITLE OF INVENTION: Mutant Trichosanthin
; FILE REFERENCE: 04399/000615-USO
; CURRENT APPLICATION NUMBER: US/09/905,247
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: CN 00119553.0
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: CN 01103102.6
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 289
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; TYPE: PRT
; ORGANISM: Trichosanthes kirilowii M.
US-09-905-247-1

Query Match      99.4%; Score 1214; DB 11; Length 289;
Best Local Similarity 99.6%; Pred. No. 1e-111;
Matches 246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 60
      |||||||
DB      24  DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 83

QY      61  SVAIDVTNYYIMGYRAGDTSYFFENASATEAKYVFKDAMRKVTLPYSGNVERLQTAAGK 120
      |||||||
DB      84  SVAIDVTNYYIMGYRAGDTSYFFENASATEAKYVFKDAMRKVTLPYSGNVERLQTAAGK 143

QY      121  IRENIPGLGIPALDSAITTLFPYNNASASALMWLIQSTSEARRYFIEQIQKRVDTFTL 180
      |||||||
DB      144  IRENIPGLGIPALDSAITTLFPYNNASASALMWLIQSTSEARRYFIEQIQKRVDTFTL 203

QY      181  PSIAIISLNSWSALS KQIQIASTNNQGFESPVLINQNRVTITNVDAVGTSTNIALL 240
      |||||||
DB      204  PSIAIISLNSWSALS KQIQIASTNNQGFESPVLINQNRVTITNVDAVGTSTNIALL 263

QY      241  LNRNNMA 247
      |||||||
DB      264  LNRNNMA 270

RESULT 4
US-10-280-679B-4
; Sequence 4, Application US/10280679B
; Publication No. US20030150019A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
; FILE REFERENCE: LSB-0109-US03
; CURRENT APPLICATION NUMBER: US/10/280,679B
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 09/557,941
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 08/484,341
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/923,692
; PRIOR FILING DATE: 1992-07-31
; PRIOR APPLICATION NUMBER: 07/600,244
; PRIOR FILING DATE: 1990-10-22
; PRIOR APPLICATION NUMBER: 07/641,617
; PRIOR FILING DATE: 1991-01-16
; PRIOR APPLICATION NUMBER: 07/737,899
; PRIOR FILING DATE: 1991-07-26
; PRIOR APPLICATION NUMBER: 07/739,143
; PRIOR FILING DATE: 1991-08-01
; PRIOR APPLICATION NUMBER: 07/310,881
; PRIOR FILING DATE: 1989-02-17
; PRIOR APPLICATION NUMBER: 07/160,766
; PRIOR FILING DATE: 1988-02-26
; PRIOR APPLICATION NUMBER: 07/160,771
; PRIOR FILING DATE: 1988-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Chinese cucumber protein alpha-trichosanthin
US-10-280-679B-4

Query Match      99.3%; Score 1212; DB 14; Length 289;
Best Local Similarity 99.2%; Pred. No. 1.6e-111;
Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1  DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 60
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Db 24 DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPILRSSLPGSORALHLTNVADETI 83  
QY 61 SVADIVTNYVMYKRGADTSYFFNEASATAAKYVFDAMRKVTLPPSGYERLQTAAGK 120  
Db 84 SVADIVTNYVMYKRGADTSYFFNEASATAAKYVFDAMRKVTLPPSGYERLQTAAGK 143  
QY 121 IRENIPILGLPALDSATITLTFYNNANSASALMWLIQSTSEARARYKFEQOIGKRVDTFL 180  
Db 144 IRENIPILGLPALDSATITLTFYNNANSASALMWLIQSTSEARARYKFEQOIGKRVDTFL 203  
QY 181 PSIAIISLENSWALSKOIQIASTNNGOFESPVLINAOQRVTITNVDAVGTSTNALL 240  
Db 204 PSIAIISLENSWALSKOIQIASTNNGOFETPVVLINAOQRVITNVDAVGTSTNALL 263  
QY 241 LNRNMA 247  
Db 264 LNRNMA 270  
RESULT 5  
US-10-280-725B-4  
; Sequence 4, Application US/10280725B  
; Publication No. US20040049025A1  
; GENERAL INFORMATION:  
; APPLICANT: Large Scale Biology Corporation  
; TITLE OF INVENTION: Recombinant Viral Nucleic Acids  
; FILE REFERENCE: LSBC-0109-US02  
; CURRENT APPLICATION NUMBER: US/10/280,725B  
; PRIOR FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: 09/557,941  
; PRIOR FILING DATE: 2000-04-24  
; PRIOR APPLICATION NUMBER: 08/484,341  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 07/923,692  
; PRIOR FILING DATE: 1992-07-31  
; PRIOR APPLICATION NUMBER: 07/600,244  
; PRIOR FILING DATE: 1990-10-22  
; PRIOR APPLICATION NUMBER: 07/641,617  
; PRIOR FILING DATE: 1991-01-16  
; PRIOR APPLICATION NUMBER: 07/737,899  
; PRIOR FILING DATE: 1991-07-26  
; PRIOR APPLICATION NUMBER: 07/739,143  
; PRIOR FILING DATE: 1991-08-01  
; PRIOR APPLICATION NUMBER: 07/310,881  
; PRIOR FILING DATE: 1989-02-17  
; PRIOR APPLICATION NUMBER: 07/160,766  
; PRIOR FILING DATE: 1988-02-26  
; PRIOR APPLICATION NUMBER: 07/160,771  
; PRIOR FILING DATE: 1988-02-26  
; Remaining prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 289  
; TYPE: PRT  
; ORGANISM: Chinese cucumber  
US-10-280-725B-4  
Query Match 99.3%; Score 1212; DB 15; Length 289;  
Best Local Similarity 99.2%; Pred. No. 1.6e-111;  
Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPILRSSLPGSORALHLTNVADETI 60  
Db 24 DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPILRSSLPGSORALHLTNVADETI 83  
QY 61 SVADIVTNYVMYKRGADTSYFFNEASATAAKYVFDAMRKVTLPPSGYERLQTAAGK 120  
Db 84 SVADIVTNYVMYKRGADTSYFFNEASATAAKYVFDAMRKVTLPPSGYERLQTAAGK 143  
QY 121 IRENIPILGLPALDSATITLTFYNNANSASALMWLIQSTSEARARYKFEQOIGKRVDTFL 180

Db 144 IRENIPILGLPALDSATITLTFYNNANSASALMWLIQSTSEARARYKFEQOIGKRVDTFL 203  
QY 181 PSIAIISLENSWALSKOIQIASTNNGOFESPVLINAOQRVTITNVDAVGTSTNALL 240  
Db 204 PSIAIISLENSWALSKOIQIASTNNGOFETPVVLINAOQRVITNVDAVGTSTNALL 263  
QY 241 LNRNMA 247  
Db 264 LNRNMA 270  
RESULT 6  
US-10-127-890-6  
; Sequence 6, Application US/10127890  
; Publication No. US20030166196A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Carroll, Stephen F.  
; Studnicka, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; Proteins  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/127,890  
; FILING DATE: 23-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,360  
; FILING DATE: 13-MAY-1996  
; APPLICATION NUMBER: PCT/US94/05348  
; FILING DATE: 12-MAY-1994  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-127-890-6  
Query Match 99.0%; Score 1209; DB 14; Length 247;  
Best Local Similarity 99.2%; Pred. No. 2.6e-111;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPILRSSLPGSORALHLTNVADETI 60

|||||  
Db 1 DVSPRLSGATSSSYGVFISNLKALPNERKLYDIPILRSLSLPGSQRYVALHLTNVADETI 60  
QY 61 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120  
Db 61 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120  
QY 121 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARARYFIEQOIGKRVDTFL 180  
Db 121 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARARYFIEQOIGKRVDTFL 180  
QY 181 PSIAIISLENSWSALSQKQIQIASTNNGQFESPVLINAGNQVATITNVDAVVTSNIALL 240  
Db 181 PSIAIISLENSWSALSQKQIQIASTNNGQFESPVLINAGNQVATITNVDAVVTSNIALL 240  
QY 241 LNRNNMA 247  
Db 241 LNRNNMA 247

## RESULT 7

US-10-717-243-6  
Sequence 6, Application US/10717243  
Publication No. US20050054835A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
Carroll, Stephen F.  
Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/717,243  
FILING DATE: 18-Nov-2003  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/839,765  
FILING DATE: 15-APR-1997  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 33,918  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-717-243-6

Query Match 99.0%; Score 1209; DB 17; Length 247;  
Best Local Similarity 99.2%; Pred. No. 2,6e-11;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVSPRLSGATSSSYGVFISNLKALPNERKLYDIPILRSLSLPGSQRYVALHLTNVADETI 60  
Db 1 DVSPRLSGATSSSYGVFISNLKALPNERKLYDIPILRSLSLPGSQRYVALHLTNVADETI 60  
QY 61 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120  
Db 61 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120  
QY 121 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARARYFIEQOIGKRVDTFL 180  
Db 121 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARARYFIEQOIGKRVDTFL 180  
QY 181 PSIAIISLENSWSALSQKQIQIASTNNGQFESPVLINAGNQVATITNVDAVVTSNIALL 240  
Db 181 PSIAIISLENSWSALSQKQIQIASTNNGQFESPVLINAGNQVATITNVDAVVTSNIALL 240  
QY 241 LNRNNMA 247  
Db 241 LNRNNMA 247

## RESULT 8

US-09-792-793a-34  
Sequence 34, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
Coghins, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
FILE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 34  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Bryonia dioica  
US-09-792-793a-34

Query Match 87.7%; Score 1071; DB 9; Length 247;  
Best Local Similarity 86.2%; Pred. No. 1.2e-97;  
Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVSPRLSGATSSSYGVFISNLKALPNERKLYDIPILRSLSLPGSQRYVALHLTNVADETI 60  
Db 1 DVSPRLSGATSSSYGVFISNLKALPNERKLYDIPILRSLSLPGSQRYVALHLTNVADETI 60  
QY 61 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120  
Db 61 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120  
QY 121 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARARYFIEQOIGKRVDTFL 180  
Db 121 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARARYFIEQOIGKRVDTFL 180  
QY 181 PSIAIISLENSWSALSQKQIQIASTNNGQFESPVLINAGNQVATITNVDAVVTSNIALL 240  
Db 181 PSIAIISLENSWSALSQKQIQIASTNNGQFESPVLINAGNQVATITNVDAVVTSNIALL 240  
QY 241 LNRNNMA 247  
Db 241 LNRNNMA 247



RESULT 9  
US-10-375-209A-34  
Sequence 34, Application US/10375209A  
Publication No. US20030215421A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
FILE REFERENCE: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
CURRENT APPLICATION NUMBER: US/10/375, 209A  
CURRENT FILING DATE: 2003-02-24  
NUMBER OF SEQ. ID NOS: 93  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 34  
LENGTH: 247  
TYPE: PRN  
ORGANISM: Bryonia dioica  
US-10-375-209A-34

Query Match 87.7%; Score 1071; DB 15; Length 247;  
Best Local Similarity 86.2%; Pred. No. 1.2e-97;  
Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISLURKALPNERKLYDIPILRSSLPQSORYALHNTYADETI 60  
1 DVSFRLSGATSSSYGVFISLURKALPNERKLYDIPILRSSLPQSORYALHNTYADETI 60  
Db 1 DVSFRLSGATSSSYGVFISLURKALPNERKLYDIPILRSSLPQSORYALHNTYADETI 60

QY 61 SVADVTNVIYIMGYADTSYFENEASATEAKVFDARKVTLTPYSGYVERLOQAAGK 120  
61 SVADVTNVIYIMGYADTSYFENEASATEAKVFDARKVTLTPYSGYVERLOQAAGK 120  
Db 61 SVADVTNVIYIMGYADTSYFENEASATEAKVFDARKVTLTPYSGYVERLOQAAGK 120

QY 121 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEARVYKFIHQIGKRVDTFL 180  
121 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEARVYKFIHQIGKRVDTFL 180  
Db 121 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEARVYKFIHQIGKRVDTFL 180

QY 181 PSLATISLENSMGSLSKQIOIASTNNGOPESPVLINAGNORVTITNVDAVGTSTNIAL 240  
181 PSLATISLENSMGSLSKQIOIASTNNGOPESPVLINAGNORVTITNVDAVGTSTNIAL 240  
Db 181 PSLATISLENSMGSLSKQIOIASTNNGOPESPVLINAGNORVTITNVDAVGTSTNIAL 240

QY 241 LNENNA 247  
241 LNENNA 247  
Db 241 LNENNA 247

RESULT 10  
US-10-127-890-7  
Sequence 7, Application US/10127890  
Publication No. US2003016196A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
Carroll, Stephen F.  
Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/127, 890  
FILING DATE: 23-Apr-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8869  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-127-890-7

Query Match 65.7%; Score 802; DB 14; Length 263;  
Best Local Similarity 65.2%; Pred. No. 6.1e-71;  
Matches 161; Conservative 37; Mismatches 49; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISLURKALPNERKLYDIPILRSSLPQSORYALHNTYADETI 60  
1 DVSFRLSGATSSSYGVFISLURKALPNERKLYDIPILRSSLPQSORYALHNTYADETI 60  
Db 1 DVSFRLSGATSSSYGVFISLURKALPNERKLYDIPILRSSLPQSORYALHNTYADETI 60

QY 61 SVADVTNVIYIMGYADTSYFENEASATEAKVFDARKVTLTPYSGYVERLOQAAGK 120  
61 SVADVTNVIYIMGYADTSYFENEASATEAKVFDARKVTLTPYSGYVERLOQAAGK 120  
Db 61 SVADVTNVIYIMGYADTSYFENEASATEAKVFDARKVTLTPYSGYVERLOQAAGK 120

QY 121 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEARVYKFIHQIGKRVDTFL 180  
121 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEARVYKFIHQIGKRVDTFL 180  
Db 121 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEARVYKFIHQIGKRVDTFL 180

QY 181 PSLATISLENSMGSLSKQIOIASTNNGOPESPVLINAGNORVTITNVDAVGTSTNIAL 240  
181 PSLATISLENSMGSLSKQIOIASTNNGOPESPVLINAGNORVTITNVDAVGTSTNIAL 240  
Db 181 PSLATISLENSMGSLSKQIOIASTNNGOPESPVLINAGNORVTITNVDAVGTSTNIAL 240

QY 241 LNENNA 247  
241 LNENNA 247  
Db 241 LNENNA 247

RESULT 11  
US-10-717-243-7  
Sequence 7, Application US/10717243  
Publication No. US20050054835A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
Carroll, Stephen F.  
Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

```

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/717,243
  FILING DATE: 18-Nov-2003
  CLASSIFICATION: 530
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/839,765
  FILING DATE: 15-APR-1997
  APPLICATION NUMBER: US 08/425,336
  FILING DATE: 18-APR-1995
  APPLICATION NUMBER: US 08/064,691
  FILING DATE: 12-MAY-1993
  APPLICATION NUMBER: US 07/988,430
  FILING DATE: 09-DEC-1992
  APPLICATION NUMBER: US 07/901,707
  FILING DATE: 19-JUN-1992
  APPLICATION NUMBER: US 07/787,567
  FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
  NAME: McNicholas, Janet M.
  REGISTRATION NUMBER: 32,918
  REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 312/707-8889
  TELEFAX: 312/707-9155
  TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 7:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 263 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-717-243-7

Query Match          65.7% Score 802; DB 17; Length 263;
Best Local Similarity 65.2% Pred. No. 6.1e-71;
Matches 161; Conservative 37; Mismatches 49; Indels 0; Gaps 0;

Cy 1 DVSFRLSGATSSSYVFNISNLRKALPNRKYLDYDPLASSLPGSGRYALIHLYTRADETI 60
Db 1 DVSFRLSGADPRSYCMFKIDLRLNALPFEKRYNIPLLPSVSGAGRYILMLFNYDGKTI 60
Cy 61 SVAIDVTWVYIMGYAGDTSYVFENFASATEAKYVFXDAMRKVTLPSGANYERLOTAGX 120
Db 61 TVAADVTWVYIMGYADDTTSYFFNEPAELASQYVFRDARRKTIPLPSGANYERLOTAGX 120
Cy 121 IRENIPILGALPADAATITLFFYNNANSAASALMWLIQSTSEARVYFIEQOIGKEVDKTF 180
Db 121 PREKIPILGALPADAISTLTLHVDSTPAAGALLVLITQTAAEARFYIEQOIGERAYRDEV 180
Cy 181 PSLAIISENSWSALSKOIQTASTNGQFESRVVLINAMQRYTTTNVDAGVTSNIMLL 240
Db 181 PSLAIISENSWSGLSKOIQLAQGNNGIFRPTIVLVDNKGRVQITTNVTSKVTYSNIOLL 240
Cy 241 LNRNNMA 247
Db 241 LNRNIA 247

RESULT 12
US-10-127-890-5
; Sequence 5, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carcoll, Stephen F.
; Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

```

```

? NUMBER OF SEQUENCES: 173
? PROTEINS
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: McAndrews, Held & Malloy, Ltd.
? STREET: 500 West Madison Street, 34th floor
? CITY: Chicago
? STATE: Illinois
? COUNTRY: USA
? ZIP: 60661
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.25
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/10/127,890
? FILING DATE: 23-Apr-2002
? CLASSIFICATION: <Unknown>
?
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/646,360
? FILING DATE: 13-MAY-1996
? APPLICATION NUMBER: PCT/US94/05348
? FILING DATE: 12-MAY-1994
? APPLICATION NUMBER: US 08/064,691
? FILING DATE: 12-MAY-1993
? APPLICATION NUMBER: US 07/988,430
? FILING DATE: 09-DEC-1992
? APPLICATION NUMBER: US 07/901,707
? FILING DATE: 19-JUN-1992
? APPLICATION NUMBER: US 07/787,567
? FILING DATE: 04-NOV-1991
?
? ATTORNEY/AGENT INFORMATION:
? NAME: McNicholas, Janet M.
? REGISTRATION NUMBER: 32,918
? REFERENCE/DOCKET NUMBER: 200-70.P4
?
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312/707-8889
? TELEFAX: 312/707-9155
?
? TELEX: 650 388-1248
?
? INFORMATION FOR SEQ ID NO: 5:
?
? SEQUENCE CHARACTERISTICS:
? LENGTH: 248 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
?
? MOLECULE TYPE: protein
?
? SEQUENCE DESCRIPTION: SEQ ID NO: 5:
?
US-10-127-890-5
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Query Match 59.3%; Score 724.5; DB 14; Length 248;
Best Local Similarity 59.0%; Pred. No. 2.7e-63;
Matches 147; Conservative 49; Mismatches 50; Indels 3; Gaps 3
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1 DVSRFLSGATSSSYGVFISNLRKALPNRKRKYDIPILRSSLPGSQRYVALIHLYTNVADETI 60
1 DVRSISLSSSSSTYSKFIQDLRKALPSNGTYVYNLIILSSASGASRYTILMTLSNDGKAI 60
?
61 SVAIDYINVTYMGTRAGDTSYFENFASLTKAAYFKDAMRKVTLPYSGNRYRLQTAACK 120
61 TVAADVDSQLYTMGLVNSTSYFFENSDAKLASQYVFKGS-TIVTLPYSGNVEKQTAAGK 119
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121 IRENPIPLCLPALDSAITTLFFYYNNANSASALMLVLQSTSEARARYKFIQOIGKRVDPKL 180
121 IREKIPILGFPALDSALITTFHYDSTAAALAAFLVILQTTAAASRFYIEGQIIRISKQNV 179
?
181 PSGLAIISSLENS-WSGLSKQIQIASTINNGQFESSPVLLINAQNRVTITNVDAQVTSNIAL 239
180 PSLATIISLENSLWSALSKQIQIQAQTNGNTFFKTPPVVITDDKQQRVEITNVTSKVTKNIQL 239
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240 LLN-RNNMA 247
240 LLL : : :
240 LLNRYQNVYA 248

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## RESULT 13

US-10-717-243-5

; Sequence 5, Application US/10717243  
; Publication No. US20050054635A1

GENERAL INFORMATION:

APPLICANT: Better, Marc D.  
Carroll, Stephen F.  
Studnicka, Gary M.TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held &amp; Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/717,243

FILING DATE: 18-Nov-2003

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/839,765

FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 5:

LENGTH: 248 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-717-243-5

Query Match

Best Local Similarity 59.3%; Score 724.5; DB 17; Length 248;

Matches 147; Conservative 49; Mismatches 50; Indels 3; Gaps 3;

QY

1 DVDFRSGATSSSYGVFISNRKALPNERKLYDIPILRSLSPGSQRYALHLTNVADDTI 60

1 DVDFRSGATSSSYGVFISNRKALPNERKLYDIPILRSLSPGSQRYALHLTNVADDTI 60

1 DVDFRSGATSSSYGVFISNRKALPNERKLYDIPILRSLSPGSQRYALHLTNVADDTI 60

1 DVDFRSGATSSSYGVFISNRKALPNERKLYDIPILRSLSPGSQRYALHLTNVADDTI 60

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1 DVDFRSGATSSSYGVFISNRKALPNERKLYDIPILRSLSPGSQRYALHLTNVADDTI 60

## RESULT 14

US-10-127-890-4

; Sequence 4, Application US/10127890  
; Publication No. US20030166196A1

GENERAL INFORMATION:

APPLICANT: Better, Marc D.  
Carroll, Stephen F.  
Studnicka, Gary M.TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held &amp; Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 4:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-127-890-4

Query Match

Best Local Similarity 61.6%; Score 709; DB 14; Length 263;

Matches 149; Conservative 30; Mismatches 61; Indels 2; Gaps 2;

QY

1 DVDFRSGATSSSYGVFISNRKALPNERKLYDIPILRSLSPGSQRYALHLTNVADDTI 60

1 DVDFRSGATSSSYGVFISNRKALPNERKLYDIPILRSLSPGSQRYALHLTNVADDTI 60

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DB 61 SVAIDVTNVIYVVAARRRDVSYFFKE-SPEPAIVILK-GRKTLTYLYTNGYENLQTPAAK 118
OY 121 IRENIPLGIPALDSAITTLTFYNNANSASALMWLIQSTSEAAKYFEQOIGKRVDTPL 180
DB 119 IRENIDLGIPALSSAITTLTFYNAQSPALTLVLIQTAAAPAFKXIERHVAKYVATNFK 178
OY 181 PSIAITLSNMSALSLSKOQIASNTNGQESPVVLINAQNRITINVDAGVYTSNALL 240
DB 179 PLIAITLSLENQWALSLSKOIFLAQNGGKFRNPVDLIKIGTERPQVYNVDSVVGKNIKLL 238
OY 241 LN 242
DB 239 LN 240

RESULT 15
US-10-717-243-4
; Sequence 4, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Belter, Marc D.
; Carroll, Stephen F.
; Studenka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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US-10-717-243-4	
Query Match	58.1%; Score 709; DB 17; Length 263;
Beet Local Similarity	61.6%; Pred. No. 1e-61;
Matches 149; Conservative	30; Mismatches 61; Indels 2; Gaps 2
QY	1 DVSFRLSGATSSSYGVFISNLRKALPNRKKYIDIPLRLSSLPQSOYALIHNTNVADETI 60
Db	1 DVNFPLSTAIKTYKFIEDFRATLPESHKVIDIPLLSTISDSRRFILMDITSAYETI 60
QY	61 SVADIVTWYIMGVPRAGDTSYFFENASATEAKYVFKDAMRKVTLTPYSGNERLTQTAAK 120
Db	61 SVADIVTWYVAYAYRTDVSYPFKE-SPEEAINILFK-GTRKILTPYTCNENYENLTQTAARK 118
QY	121 IRENIPGLPALDSAITTLTFYNNANSAASALMWLIQSTSEARYKFIQEOIGKRVDTFL 180
Db	119 IRENIDLGIPALSSAITLTFEYNNAGSAPSAIIVLIQTAAEARPKYIEBHVAKYAVATNFK 178
QY	181 PSLAIISSENKWSALSKOIQIASTNNGQEPESPVYLINANONRVITTNPDAGVYTSIALLL 240
Db	179 PNLAIISLENOWSALSKOIFLAONOGKFRNPVDLIKPTGERFOVTNWDSDVVKIGIKILL 238
QY	241 LN 242
Db	239 LN 240

Search completed: April 12, 2005, 15:31:53  
Job time : 82.5653 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2005, 14:56:17 ; Search time 106.91 Seconds

(without alignments)  
1183.080 Million cell updates/sec

Title: US-09-905-247A-8

Perfect score: 1221

Sequence: 1 DVSGFRLSGATSSSYGVFISN.....VDAGVTSNIALLNENNA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1221	100.0	289	1	RIP1 TRIKI
2	1218	99.8	289	1	RIP1 TRIKI
3	1217	99.7	289	2	Q94K58
4	1207	98.9	289	2	Q94K54
5	1195	97.9	247	2	Q41216
6	1194	97.8	289	2	Q6B8Q4
7	1187	97.2	247	2	RIPS TRIKI
8	1162	95.2	270	2	Q91RE3
9	1162	95.2	270	2	Q41611
10	1158	94.8	270	2	Q6PRG5
11	1071	87.7	290	1	Q8LPI7
12	802	65.7	286	1	RIP1 BRYDI
13	754	61.8	277	2	RIP1 MOMCH
14	728.5	59.7	278	2	RIP1 LURCY
15	711	58.2	264	2	Q00980
16	711	58.2	264	2	Q68405
17	709	58.1	286	1	RIP3 MOMCH
18	691.5	56.6	286	1	RIP2 MOMBA
19	680	55.7	250	1	RIP1 CUCFI
20	644.5	52.8	294	1	RIP1 TRIAN
21	535	43.8	282	1	RIP2 BRYDI
22	476.5	39.0	136	2	Q8SAD7
23	425.5	34.8	563	2	Q8G1T2
24	425	34.8	541	2	Q41174
25	421	34.5	576	1	RICI RICCO
26	420.5	34.4	563	2	RICI SAMNI
27	420.5	34.4	563	2	Q94S82
28	419.5	34.4	563	2	Q04367
29	417.5	34.2	275	2	Q8H1Y4
30	415.5	34.0	136	2	Q8SAG0
31	412.5	33.8	580	2	Q94BW4

32	408.5	33.5	580	2	Q94BM3	Q94Bw3 cinamomum
33	407.5	33.4	275	2	Q84LJ1	Q84Lj1 gnostemma
34	405.5	33.2	581	2	Q94BWS	Q94Bws cinamomum
35	404.5	33.1	564	2	Q94VR2	Q94Vr2 sambucus eb
36	403.5	33.0	277	2	Q8GV09	Q8GV09 gnostemma
37	403.5	33.0	549	2	Q9FV22	Q9Fv22 cinamomum
38	401.5	32.9	277	2	Q84VR1	Q84Vr1 gnostemma
39	400.5	32.8	277	2	Q8GV11	Q8GV11 gnostemma
40	396.5	32.5	564	1	AGSL RICCO	P06750 ricinus com
41	395.5	32.4	277	2	Q8H1Y5	Q8H1Y5 gnostemma
42	393.5	32.2	136	2	Q84LJ0	Q84Lj0 cucurbita m
43	392.5	32.1	136	2	Q84LI9	Q84Li9 cucurbita m
44	388.5	31.8	277	2	Q8GV10	Q8GV10 gnostemma
45	384.5	31.5	136	2	Q8S2R5	Q8S2r5 cucurbita m

## ALIGNMENTS

RESULT 1	ID	RIP1 TRIKI	STANDARD;	PRT;	289 AA.
AC	P09889;				
DT	01-MAR-1989 (Rel. 10, Created)				
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Ribosome-inactivating protein alpha-trichosanthin precursor				
DE	(EC 3.2.2.22) (tRNA N-glycosidase) (Alpha-TCS).				
OS	Trichosanthin kirkii (Mongolian snake-gourd).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;				
OC	Eurosid I; Cucurbitales; Cucurbitaceae; Trichosanthes.				
OX	NCBI_TaxID=3677;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Maximowicz;				
RX	MEDLINE=91153657; PubMed=1999291; DOI=10.1016/0378-1119(91)90061-F;				
RA	Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;				
RT	"Cloning of trichosanthin cDNA and its expression in Escherichia				
RT	coli.";				
RL	Gene 97:267-272 (1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Maximowicz; TISSUE=leaf;				
RX	MEDLINE=90256790; PubMed=2341400;				
RA	Chow T., Feldman R.A., Lovett M., Piatek M.;				
RT	"Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a				
RT	type I ribosome-inactivating protein.";				
RL	J. Biol. Chem. 265:8670-8674 (1990).				
RN	[3]				
RP	SEQUENCE OF 24-270.				
RC	STRAIN=Maximowicz; TISSUE=tuberous root;				
RX	MEDLINE=90256789; PubMed=2341399;				
RA	Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,				
RT	Wu P., Hwang K., Piatek M.;				
RT	"Primary amino acid sequence of alpha-trichosanthin and molecular				
RT	models for abrin A-chain and alpha-trichosanthin.";				
RL	J. Biol. Chem. 265:8665-8669 (1990).				
RN	[4]				
RP	TISSUE=tuberous root;				
RC	Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,				
RA	Tian G.Y., Ni C.Z.;				
RT	"Scientific evaluation of Tian Hua Fen (THF): history, chemistry and				
RT	application.";				
RL	Pure Appl. Chem. 58:789-798 (1996).				
RN	[5]				
RP	X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).				
RX	MEDLINE=94344957; PubMed=806085;				
RA	Zhou F., Fu Z., Chen M., Lin Y., Pan K.;				
RT	"Structure of trichosanthin at 1.88-A resolution.";				
RL	Proteins 19:4-13 (1994).				
RN	[6]				

RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RA MEDLINE=95344383; PubMed=7619070;  
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;  
 RT "Studies on crystal structures, active-centre geometry and  
 RT dephasing mechanism of two ribosome-inactivating proteins";  
 RL Biochem J 309:285-298(1995).  
 CC -!- FUNCTION: Trichosanthin is an abortion-inducing protein. It is  
 CC capable of inhibiting HIV-1 infection and replication. It  
 CC inactivates eukaryotic 60S ribosomal subunits.  
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
 CC Type 1 RIP subfamily.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M34858; AAA34207.1; -;  
 DR EMBL: J05434; AAA34206.1; -;  
 DR PIR: J70566; RLITZT.  
 DR PDB: 1GIS; X-ray; A=23-270.  
 DR PDB: 1GIU; X-ray; A=24-270.  
 DR PDB: 1J4G; X-ray; A/B/C/D=23-270.  
 DR PDB: 1MRJ; X-ray; @=24-270.  
 DR PDB: 1MRK; X-ray; @=24-270.  
 DR PDB: 1NLI; X-ray; A=23-270.  
 DR PDB: 1QD2; X-ray; A=24-270.  
 DR PDB: 1TCS; X-ray; @=24-270.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
 KW 3D-structure; Antiviral; Direct protein sequencing; Hydrolase;  
 KW Plant defense; Protein synthesis inhibitor; Signal; Toxin.  
 FT CHAIN 1 23  
 FT SIGNAL 24 270  
 FT PROPEP 271 289  
 FT ACT\_SITE 183 183  
 FT CONFLICT 57 60  
 FT CONFLICT 82 84  
 FT CONFLICT 87 87  
 FT CONFLICT 92 92  
 FT CONFLICT 143 144  
 FT CONFLICT 196 196  
 FT CONFLICT 215 216  
 FT CONFLICT 231 231  
 FT CONFLICT 234 234  
 FT CONFLICT 246 266  
 FT CONFLICT 247 247  
 FT STRAND 25 28  
 FT TURN 30 31  
 FT HELIX 34 46  
 FT TURN 47 47  
 FT STRAND 50 54  
 FT TURN 55 56  
 FT STRAND 57 60  
 FT HELIX 66 69  
 FT STRAND 70 76  
 FT TURN 78 79  
 FT STRAND 82 88  
 FT TURN 89 92  
 FT STRAND 93 99  
 FT TURN 100 101  
 FT STRAND 102 105  
 FT HELIX 109 114  
 FT TURN 115 117  
 FT TURN 120 121

Removed in mature form.  
 By similarity.  
 IPR -> IPR1 (in Ref. 4).  
 Missing (in Ref. 4).  
 I -> L (in Ref. 4).  
 V -> VDAIIPRNAV (in Ref. 4).  
 KI -> GL (in Ref. 4).  
 K -> S (in Ref. 4).  
 WS -> LML (in Ref. 4).  
 Q -> T (in Ref. 4).  
 S -> T (in Ref. 2).  
 Missing (in Ref. 4).  
 T -> W (in Ref. 2).  
 Ribosome-inactivating protein alpha-trichosanthin.

FT STRAND 124 127  
 FT HELIX 134 141  
 FT TURN 142 142  
 FT HELIX 145 147  
 FT STRAND 150 150  
 FT HELIX 152 163  
 FT TURN 164 165  
 FT HELIX 167 180  
 FT TURN 181 181  
 FT HELIX 182 186  
 FT STRAND 187 187  
 FT HELIX 188 195  
 FT TURN 196 196  
 FT STRAND 202 202  
 FT HELIX 206 226  
 FT TURN 227 230  
 FT STRAND 231 239  
 FT TURN 241 242  
 FT STRAND 245 250  
 FT TURN 251 252  
 FT HELIX 254 258  
 FT TURN 259 259  
 FT STRAND 260 260  
 FT STRAND 263 263  
 FT TURN 266 268  
 SQ SEQUENCE 289 AA; 31676 MW; 5CE09BB630575BB9 CRC64;  
 Query Match 100.0%; Score 1221; DB 1; Length 289;  
 Best Local Similarity 100.0%; Pred. No. 4,7e-92;  
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKYDIPLRSSLPQSGRYALIHITNYADETI 60  
 DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKYDIPLRSSLPQSGRYALIHITNYADETI 83  
 QY 61 SVAIDVTNYITNGYAGGTSYFENASATBAKYFKDAMKRYTPYSGNTERLQTAAGK 120  
 DB 84 SVAIDVTNYITNGYAGGTSYFENASATBAKYFKDAMKRYTPYSGNTERLQTAAGK 143  
 QY 121 IRENIPGLPALDASITTLFYNNANSAASALMWLIQSTSEARYYFIEQIGKVDKFTL 180  
 DB 144 IRENIPGLPALDASITTLFYNNANSAASALMWLIQSTSEARYYFIEQIGKVDKFTL 203  
 QY 181 PSLAIIISLNSNSALSKQIQIASTNNGQFESPVLINQORVITTNVADGVTSNIALL 240  
 DB 204 PSLAIIISLNSNSALSKQIQIASTNNGQFESPVLINQORVITTNVADGVTSNIALL 263  
 QY 241 LNRNNMA 247  
 DB 264 LNRNNMA 270  
 RESULT 2  
 Q84SV8 PRELIMINARY; PRT; 289 AA.  
 AC Q84SV8;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Trichosanthin.  
 GN Name=TCS;  
 OS Trichosanthes kirilowii (Mongolian snake-gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.  
 OC NCBI\_TaxID=3677;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yuan H., Wang L., Wang Y., Liu T., An C., Chen Z.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.

DR EMBL: AY082349; AA072728.1; -  
DR HSBP; P09989; IMRT.  
DR GO:0016787; F:hydrolyase activity; IEA.  
DR GO:0030598; F:RNA N-glycosylase activity; IEA.  
DR GO:0006952; P:defense response; IEA.  
DR GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
DR GO:0009405; P:pathogenesis; IEA.  
DR InterPro: IPR001574; RIF.  
DR Pfam: PF00161; RIF; 1.  
DR PRINTS; PR00396; SHIGARICIN.  
DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
KW Hydrolyase; Plant defense; Protein synthesis inhibitor; Toxin.  
SQ SEQUENCE 289 AA, 31650 MM; B403148E96861FA CRC64;  
  
Query Match 99.8%; Score 1218; DB 2; Length 289;  
Best Local Similarity 99.6%; Pred. No. 8.3e-92;  
Matches 246; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DVSFPLSGATSSSYGVFTISNRKALPNBRKYDIPILNSSLPGSORVALIHLTNVADFTI 60  
DB |||||  
QY 24 DVSFPLSGATSSSYGVFTISNRKALPNBRKYDIPILNSSLPGSORVALIHLTNVADFTI 83  
DB |||||  
QY 61 SVADIVTVYIMGVAGDTSVFENASATEAKYVFKAMRVTLPSVAGNERLOTAGK 120  
DB SVADIVTVYIMGVAGDTSVFENASATEAKYVFKAMRVTLPSVAGNERLOTAGK 143  
QY 121 IRENPLGLPALDSAITTLFYNNASASALMWLIQSTSEARFYFICQIGKRVDTFL 180  
DB IRENPLGLPALDSAITTLFYNNASASALMWLIQSTSEARFYFICQIGKRVDTFL 203  
QY 144 IRENPLGLPALDSAITTLFYNNASASALMWLIQSTSEARFYFICQIGKRVDTFL 203  
DB IRENPLGLPALDSAITTLFYNNASASALMWLIQSTSEARFYFICQIGKRVDTFL 263  
QY 181 PSLAIISLNSWSALSQIQIASTNNGQFESFPVLINQORVTTITNVADGVTSNIAL 240  
DB PSLAIISLNSWSALSQIQIASTNNGQFESFPVLINQORVTTITNVADGVTSNIAL 263  
QY 204 PSLAIISLNSWSALSQIQIASTNNGQFESFPVLINQORVTTITNVADGVTSNIAL 263  
DB PSLAIISLNSWSALSQIQIASTNNGQFESFPVLINQORVTTITNVADGVTSNIAL 263  
QY 241 LNRNMA 247  
DB |||||  
QY 264 LNRNMA 270  
DB |||||  
  
RESULT 3  
Q94KE4 PRELIMINARY; PRT. 289 AA.  
AC Q94KE4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Trichosanthin precursor.  
GN Name=ICS;  
OS Trichosanthes kirilowii (Mongolian snake-gourd).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eustosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.  
OX NCB1\_TaxID=3677;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yuan H., Wang L., Wang Y., An C., Chen Z.;  
RL Submitted (Mar-2001) to the EMBL/Genbank/DDBJ databases.  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
CC specific adenosine on the 28S rRNA.  
CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
DR EMBL; AF367252; AA052960.1; -  
DR PIR; JC5032; JC5032.  
DR HSSP; P09989; IMRT.  
DR GO:0016787; F:hydrolyase activity; IEA.  
DR GO:0030598; F:RNA N-glycosylase activity; IEA.  
DR GO:0006952; P:defense response; IEA.  
DR GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
DR InterPro: IPR001574; RIF.  
DR Pfam; PF00161; RIF; 1.  
DR PRINTS; PR00396; SHIGARICIN.  
DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
KW Hydrolyase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.

FT	SIGNAL	1	23	Potential.
FT	CHAIN	24	270	trichosanthin.
SD	SEQUENCE	289 AA;	31706 MW;	AAD5602549CA5657 CRC64;
Query Match		99.7%;	Score 1217;	DB 2;
Best Local Similarity		99.2%;	Pred. No. 1e-91;	Length 289;
Matches	245;	Conservative	2;	Mismatches 0;
			Indels	0;
			Gaps	0
QY		1	DVSRFLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGSQRYALIHLTNYADETI	60
DB		24	DVSRFLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGSQRYALIHLTNYADETI	83
QY		61	SVAIDVTNVTYIMGRAGDTSYFENEASATEAKYVFKAMRKVTLPYSGNTERLQTAAGK	120
DB		84	SVAIDVTNVTYIMGRAGDTSYFENEASATEAKYVFKDSMKRITLPYSGNTERLQTAAGK	143
QY		121	IRENIPGLPLDSDAITTLTFYNNNSASALMWLIQSTSEARVYKFIQOIGKRDYKFL	180
DB		144	IRENIPGLPLDSDAITTLTFYNNNSASALMWLIQSTSEARVYKFIQOIGKRDYKFL	203
QY		181	PSLAIIISLNSWSALSKOIQIASTNNGCFESPVLINQONRVITTNDAVTSINALL	240
DB		204	PSLAIIISLNSWSALSKOIQIASTNNGCFESPVLINQONRVITTNDAVTSINALL	263
QY		241	LNRRNMA 247	
DB		264	LNRRNMA 270	
RESULT 4				
Q41216				
ID	Q41216	PRELIMINARY;	PRT;	289 AA.
AC	Q41216;			
DT	01-NOV-1996 (TREMREL. 01. Created)			
DT	01-NOV-1996 (TREMREL. 01. Last sequence update)			
DT	01-OCT-2003 (TREMREL. 25. Last annotation update)			
DE	Trichosanthin.			
GN	Name=trichosanthin; Synonyms=TCS;			
OS	Trichosanthes kirilowii (Mongolian snake-gourd).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	Eurosids 1; Cucurbitales; Cucurbitaceae; Trichosanthes.			
OX	NCBI_TaxID=3677;			
RN	[1]			
RP	SEQUENCE FROM N. A.			
RX	MEDLINE=94271613; PubMed=8003348;			
RA	Zheng H., Wang B., Shaw P., Yeung H.;			
RT	"Cloning and DNA sequencing of the gene encoding trichosanthin.";			
RL	I Chuan Hsueh Pu 21:42-51(1994).			
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one			
CC	specific adenosine on the 285 rRNA.			
CC	-1- SIMILARITY: Belongs to the ribosome-inactivating protein family.			
DR	EMBL; S70176; AAB31048.1; -.			
DR	PIR; JCS032; JCS032.			
DR	HSSP; P09989; J04G.			
DR	GO; GO:0030598; P:negative regulation of protein biosynthesis; IEA.			
DR	GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.			
DR	InterPro; IPR001574; R1P.			
DR	Pfam; PF00161; R1P; 1.			
DR	PRINTS; PR00396; SHGARICIN.			
DR	PROSITE; PS00275; SHGA_RICIN; 1.			
KW	Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.			
SD	SEQUENCE 289 AA; 31650 MW; 266AC14D8BCA175 CRC64;			
Query Match		98.9%;	Score 1207;	DB 2;
Best Local Similarity		98.4%;	Pred. No. 6.6e-91;	Length 289;
Matches	243;	Conservative	4;	Mismatches 0;
			Indels	0;
			Gaps	0
QY		1	DVSRFLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGSQRYALIHLTNYADETI	60
DB		24	DVSRFLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGSQRYALIHLTNYADETI	83
QY		61	SVAIDVTNVTYIMGRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNTERLQTAAGK	120
DB		84	SVAIDVTNVTYIMGRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNTERLQTAAGK	143
QY		121	IRENIPGLPLDSDAITTLTFYNNNSASALMWLIQSTSEARVYKFIQOIGKRDYKFL	180
DB		144	IRENIPGLPLDSDAITTLTFYNNNSASALMWLIQSTSEARVYKFIQOIGKRDYKFL	203
QY		181	PSLAIIISLNSWSALSKOIQIASTNNGCFESPVLINQONRVITTNDAVTSINALL	240
DB		204	PSLAIIISLNSWSALSKOIQIASTNNGCFESPVLINQONRVITTNDAVTSINALL	263
QY		241	LNRRNMA 247	
DB		264	LNRRNMA 270	

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Db      84  SVAIDVTSYIMGVDTSYFENEASATEAKYFKDARKKTLTPYSGYERLQTPAAG 143
      121  IRENIPILGIPALDSATITLTPYVANSASALMWLIQSTSPAAKYKFEQOIGKRVKTF 180
      144  IRENIPILGIPALDSATITLTPYVANSASALMWLIQSTSPAAKYKFEQOIGKRVKTF 203
Qy      181  PSIAITISLENSWALSKEQIOIASTNNQGFESPVVLINAGQRTITNVDAVVTSNIAL 240
      204  PSIAITISLENSWALSKEQIOIASTNNQGFETPVVLINAGQRTITNVDAVVTSNIAL 263
Qy      241  LNRNNMA 247
      264  LNRNDMA 270
Db

RESULT 5
06B04 ID 06B04 PRELIMINARY; PRT; 247 AA.
AC 06B04;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Trichosanthin (Fragment).
GN Name=TC5;
OS Trichosanthes kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside 1; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=3677;
RN [1]
RP SEQUENCE FROM N.A.
RA M4 S.-L., Wang Y., Li Y.-Y., Chen Z.-L., An C.-C.;
RA "Trichosanthes kirilowii trichosanthin (TCS) mature peptide gene.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
CC EMBL: AY669811; AA791090.1; -.
DR GO: GO:0030598; F:RNA N-glycosylase activity; IEA.
DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro: IPR001574; RIF.
DR Pfam: PF00161; RIF; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolyase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 1
FT CHAIN 1
FT NON_TER <1
FT TER 247
SQ SEQUENCE 247 AA; 27172 MW; BCA762884F9CCE CRC64;

Query Match 97.9%; Score 1195; DB 2; Length 247;
Best Local Similarity 97.6%; Pred. No.5.2e-90;
Matches 241; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGQRYALHLTNVADDTI 60
      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGQRYALHLTNVADDTI 60
Db      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGQRYALHLTNVADDTI 60
Qy      61  SVAIDVTNYIMGVRGDTSYFENEASATEAKYFKDARKKTLTPYSGYERLQTPAAG 120
      61  SVAIDVTNYIMGVRGDTSYFENEASATEAKYFKDARKKTLTPYSGYERLQTPAAG 120
Db      121  IRENIPILGIPALDSATITLTPYVANSASALMWLIQSTSPAAKYKFEQOIGKRVKTF 180
      121  IRENIPILGIPALDSATITLTPYVANSASALMWLIQSTSPAAKYKFEQOIGKRVKTF 180
Qy      181  PSIAITISLENSWALSKEQIOIASTNNQGFESPVVLINAGQRTITNVDAVVTSNIAL 240
      181  PSIAITISLENSWALSKEQIOIASTNNQGFETPVVLINAGQRTITNVDAVVTSNIAL 240
Db      181  PSIAITISLENSWALSKEQIOIASTNNQGFETPVVLINAGQRTITNVDAVVTSNIAL 240
Qy      241  LNRNNMA 247
      241  LNRNNMA 247

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Db      241  LNRNNMA 247
      241  LNRNNMA 247
Db

RESULT 6
RIPS TRIKI ID RIPS TRIKI STANDARD; PRT; 289 AA.
AC P24478;
DT 01-MAR-1992 (Rel. 21, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ribosome-inactivating protein karasurin precursor (EC 3.2.2.22) (rRNA
DE N-glycosidase).
OS Trichosanthes kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside 1; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=3677;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root tuber;
RX MEDLINE=97356562; PubMed=9212998;
RA Mizukami H., Iida K., Kondo T., Ogihara Y.;
RT "Cloning and bacterial expression of a gene encoding ribosome-
RT inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes
RT kirilowii var. 'japonica.'
RL Biol. Pharm. Bull. 20:711-713 (1997).
RN [2]
RP SEQUENCE OF 24-270.
RX MEDLINE=92005921; PubMed=1914000;
RA Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
RT "The complete amino acid sequence of an abortifacient protein,
RT karasurin."
RL Chem. Pharm. Bull. 39:1244-1249 (1991).
CC -1- FUNCTION: Abortion-inducing protein. It inactivates eukaryotic 60S
CC ribosomal subunits.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
CC Type 1 RIP subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB000666; BAA21786.1; -.
DR PIR; JCS606; JCS606.
DR PIR; JU0393; JU0393.
DR HSSP; P09989; IMR1.
DR InterPro; IPR001574; RIF.
DR Pfam; PF00161; RIF; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Antiviral; Direct protein sequencing; Hydrolase; Plant defense;
KW Protein synthesis inhibitor; Signal; Toxin.
FT SIGNAL 1
FT CHAIN 21
FT CHAIN 22
FT CHAIN 270
FT CHAIN 24
FT PROTEP 271
FT ACT_SITE 183
SQ SEQUENCE 289 AA; 31704 MW; 883D3B3242887B26 CRC64;

Query Match 97.8%; Score 1194; DB 1; Length 289;
Best Local Similarity 97.6%; Pred. No.7.7e-90;
Matches 241; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGQRYALHLTNVADDTI 60
      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGQRYALHLTNVADDTI 60

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Db 24 DVSFRLSGATSSSYGVFISNLRKALPYERKLYDIPILRSTLPQSGRYALHLTNVADETI 83  
QY 61 SVAIDVTNYIMGRAGDTSYFPEFNEASATEAAKYVFKDMARKYTLTPYSGYERLQTPACK 120  
Db 84 SVAIDVTNYIMGRAGDTSYFPEFNEASATEAAKYVFKDMARKYTLTPYSGYERLQTPACK 143  
QY 121 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEARARYKFEQOIGKRVKTF 180  
Db 144 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEARARYKFEQOIGKRVKTF 203  
QY 181 PSIAIISLENSWSALSKQIOIASTNNGQFESPVLINAQNRVTITNVDAVTSNIAL 240  
Db 204 PSIAIISLENSWSALSKQIOIASTNNGQFETPVLLINAQNRVTITNVDAVTSNIAL 263  
QY 241 LNRNNMA 247  
Db 264 LNRNNMA 270

RESULT 7  
Q9LRE3 PRELIMINARY; PRT; 247 AA.  
AC Q9LRE3; 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Trichobakin (Fragment).  
GN Name=TBK;  
OS Trichosanthes sp. Bac Kan 8-98.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.  
NCBI\_TaxID=118182;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=21476888; PubMed=11592913;  
RA Van Chi P., Quoc Truong H., Thuy Ha N., Chung W.I., Binh L.T.;  
RT "Characterization of trichobakin, a type I ribosome-inactivating  
RT protein from Trichosanthes sp. Bac Kan 8-98."  
RL Biotechnol. Appl. Biochem. 34:85-92(2001).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
CC specific adenosine on the 28S rRNA.  
CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
DR EMBL: AB039324; BAA92530.1; -.  
DR HSSP: P09989; 104G.  
DR GO: GO:0016787; F:hydrolase activity; IEA.  
DR GO: GO:0030598; F:rRNA N-glycosylase activity; IEA.  
DR GO: GO:0006952; P:defense response; IEA.  
DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
DR GO: GO:0009405; P:apoptogenesis; IEA.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP; 1.  
DR PRINTS: PR00396; SHIGARICIN.  
DR PROSITE: PS00275; SHIGA RICIN; 1.  
KW Hydrolase; Plant defense; protein synthesis inhibitor; Toxin.  
FT NON\_TER 1  
FT TER 247  
SQ SEQUENCE 247 AA; 27199 MW; 89811AC32892F03F CRC64;

Query Match 97.2%; Score 1187; DB 2; Length 247;  
Best Local Similarity 97.2%; Pred. No. 2.4e-89;  
Matches 240; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPYERKLYDIPILRSTLPQSGRYALHLTNVADETI 60  
Db 1 DVSFRLSGATSSSYGVFISNLRKALPYERKLYDIPILRSTLPQSGRYALHLTNVADETI 60  
QY 61 SVAIDVTNYIMGRAGDTSYFPEFNEASATEAAKYVFKDMARKYTLTPYSGYERLQTPACK 120  
Db 61 SVAIDVTNYIMGRAGDTSYFPEFNEASATEAAKYVFKDMARKYTLTPYSGYERLQTPACK 120  
QY 121 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEARARYKFEQOIGKRVKTF 180  
Db 121 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEARARYKFEQOIGKRVKTF 180

Db 121 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEARARYKFEQOIGKRVKTF 180  
QY 181 PSIAIISLENSWSALSKQIOIASTNNGQFESPVLINAQNRVTITNVDAVTSNIAL 240  
Db 181 PSIAIISLENSWSALSKQIOIASTNNGQFETPVLLINAQNRVTITNVDAVTSNIAL 240  
QY 241 LNRNNMA 247  
Db 241 LNRNNMA 247

RESULT 8  
Q41611 PRELIMINARY; PRT; 270 AA.  
AC Q41611; 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Trichosanthes kirilowii (Mongolian snake-gourd).  
OS Trichosanthes kirilowii (Mongolian snake-gourd).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.  
NCBI\_TaxID=3677;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bao Y., Chu R., Han J., Zhang H., Pan N., Gu X., Chen Z.;  
RT "Cloning and sequencing of trichosanthin gene and its expression in  
RT Escherichia coli and tobacco plant."  
RL Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 36:669-676(10).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Xu L.;  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
CC specific adenosine on the 28S rRNA.  
CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
DR EMBL: U55675; AAA70096.1; -.  
DR HSSP: P09989; 1MRU.  
DR GO: GO:0016787; F:hydrolase activity; IEA.  
DR GO: GO:0030598; F:rRNA N-glycosylase activity; IEA.  
DR GO: GO:0006952; P:defense response; IEA.  
DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
DR GO: GO:0009405; P:apoptogenesis; IEA.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP; 1.  
DR PRINTS: PR00396; SHIGARICIN.  
DR PROSITE: PS00275; SHIGA RICIN; 1.  
KW Hydrolase; Plant defense; protein synthesis inhibitor; Toxin.  
FT NON\_TER 270  
FT TER 270  
SQ SEQUENCE 270 AA; 29993 MW; 3D73FBA61EA8BD4 CRC64;

Query Match 95.2%; Score 1162; DB 2; Length 270;  
Best Local Similarity 94.7%; Pred. No. 3e-87;  
Matches 224; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPYERKLYDIPILRSTLPQSGRYALHLTNVADETI 60  
Db 24 DVSFRLSGATSSSYGVFISNLRKALPYERKLYDIPILRSTLPQSGRYALHLTNVADETI 83  
QY 61 SVAIDVTNYIMGRAGDTSYFPEFNEASATEAAKYVFKDMARKYTLTPYSGYERLQTPACK 120  
Db 84 SVAIDVTNYIMGRAGDTSYFPEFNEASATEAAKYVFKDMARKYTLTPYSGYERLQTPACK 143  
QY 121 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEARARYKFEQOIGKRVKTF 180  
Db 144 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEARARYKFEQOIGKRVKTF 203  
QY 181 PSIAIISLENSWSALSKQIOIASTNNGQFESPVLINAQNRVTITNVDAVTSNIAL 240  
Db 204 PSIAIISLENSWSALSKQIOIASTNNGQFETPVLLINAQNRVTITNVDAVTSNIAL 263  
QY 241 LNRNNMA 247

Db 264 INRNMA 270

## RESULT 9

Q6PRG5 PRELIMINARY; PRT; 270 AA.

AC Q6PRG5; PRELIMINARY; PRT; 270 AA.  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Trichomislin (Fragment).  
 GN Name=tcml;  
 OS Trichosanthes kirilowii (Mongolian snake-gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid1; Cucurbitales; Cucurbitaceae; Trichosanthes.  
 OC NCB1\_Taxid=3677;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Mi S., An C., Chen J., Wang Y., Yuan H., Chen Z.;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 specific adenosine on the 28S rRNA.  
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
 CC EMBL; AY584242; AAC92579.1; -.  
 DR HSSP; P16094; IABC.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
 DR GO; GO:0009405; P:negative regulation of protein biosynthesis; IEA.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.  
 FT NON TER 270  
 SQ SEQUENCE 270 AA; 29649 MW; 5BB513B754F9B769 CRC64;

Query Match 95.2%; Score 1162; DB 2; Length 270;  
 Best Local Similarity 95.5%; Pred. No. 3e-87;  
 Matches 236; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSGRYALIHLYTNADETI 60  
 DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSGRYALIHLYTNADETI 83  
 QY 61 SVAIDVTNVIYIMGYRAGDTSYFPENASATEAKYVFKDARKKVTLPYSGNYERLQTPACK 120  
 DB 84 SVAIDVTNVIYIMGYRAGDTSYFPENASATEAKYVFKDARKKVTLPYSGNYERLQTPACK 143  
 QY 121 IRENIPGLGPAIDSAITTLFFYNNANSASALMWLIVLQSTSEARRYKFIHQIGKRDVKTFL 180  
 DB 144 IRENIPGLGPAIDSAITTLFFYNNANSASALMWLIVLQSTSEARRYKFIHQIGKRDVKTFL 203  
 QY 181 PSLAIISLNSWSALSQIQIASTNNQGFESPVLINQONRVITINVDAGVTSNIALL 240  
 DB 204 PSLAIISLNSWSALSQIQIASTNNQGFESPVLINQONRVITINVDAGVTSNIALL 263  
 QY 241 INRNMA 247  
 DB 264 INRNMA 270

## RESULT 10

Q8LPV7 PRELIMINARY; PRT; 270 AA.

AC Q8LPV7; PRELIMINARY; PRT; 270 AA.  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Trichosanthin precursor (Fragment).

GN Name=TCS;  
 OS Trichosanthes kirilowii (Mongolian snake-gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid1; Cucurbitales; Cucurbitaceae; Trichosanthes.  
 OC NCB1\_Taxid=3677;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Yuan H., Wang Y., Liu T., An C., Chen Z.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 specific adenosine on the 28S rRNA.  
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
 CC EMBL; AY082348; AAM2782.1; -.  
 DR PIR; JC5032; JC5032.  
 DR HSSP; P09989; IMRI.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
 DR GO; GO:0009405; P:negative regulation of protein biosynthesis; IEA.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.  
 FT SIGNAL 1 23  
 FT CHAIN 24 >270  
 FT NON TER 270  
 SQ SEQUENCE 270 AA; 29683 MW; 531713B754F9B769 CRC64;

Query Match 94.8%; Score 1158; DB 2; Length 270;  
 Best Local Similarity 95.1%; Pred. No. 6.4e-87;  
 Matches 235; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSGRYALIHLYTNADETI 60  
 DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSGRYALIHLYTNADETI 83  
 QY 61 SVAIDVTNVIYIMGYRAGDTSYFPENASATEAKYVFKDARKKVTLPYSGNYERLQTPACK 120  
 DB 84 SVAIDVTNVIYIMGYRAGDTSYFPENASATEAKYVFKDARKKVTLPYSGNYERLQTPACK 143  
 QY 121 IRENIPGLGPAIDSAITTLFFYNNANSASALMWLIVLQSTSEARRYKFIHQIGKRDVKTFL 180  
 DB 144 IRENIPGLGPAIDSAITTLFFYNNANSASALMWLIVLQSTSEARRYKFIHQIGKRDVKTFL 203  
 QY 181 PSLAIISLNSWSALSQIQIASTNNQGFESPVLINQONRVITINVDAGVTSNIALL 240  
 DB 204 PSLAIISLNSWSALSQIQIASTNNQGFESPVLINQONRVITINVDAGVTSNIALL 263  
 QY 241 INRNMA 247  
 DB 264 INRNMA 270

## RESULT 11

RIP1\_BRYDI STANDARD; PRT; 290 AA.

AC P33185; Q9S819; STANDARD; PRT; 290 AA.  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Ribosome-inactivating protein bryodin I precursor (EC 3.2.2.22) (rRNA  
 N-glycosidase) (BDI).  
 OS Bryonia dioica (Red bryony).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid1; Cucurbitales; Cucurbitaceae; Bryonia.  
 OC NCB1\_Taxid=3652;  
 RN (1)  
 RP SEQUENCE FROM N.A., MUTAGENESIS OF GUU-212, AND X-RAY CRYSTALLOGRAPHY  
 RP (2.1 ANGSTROMS).

RC TISSUE=Leaf;  
 RX MEDLINE=97228081; Pubmed=9115985; DOI=10.1021/b1962474+;  
 RA Siegal C.B.; Neubauer M., Klei H.E., Chang C.Y.Y., Einspahr H.M.,  
 RT "Molecular, biological, and preliminary structural analysis of  
 RT recombinant bryodin 1, a ribosome-inactivating protein from the plant  
 RT Bryonia dioica.";  
 RL Biochemistry 36:3095-3103(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Siegal C.B.;  
 RT "Cloning and expression of a gene encoding bryodin 1 from Bryonia  
 RT dioica.";  
 RL Patent number US5541110, 30-JUL-1996.  
 RN [3]  
 RP SEQUENCE OF 24-66.  
 RX TISSUE=Seed;  
 RC MEDLINE=89326691; Pubmed=2753596;  
 RA Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,  
 RT Lappi D.;  
 RL "N-terminal sequence of some ribosome-inactivating proteins.";  
 RT Int. J. Pept. Protein Res. 33:263-267(1989).  
 RN [4]  
 RP SEQUENCE OF 24-43.  
 RX TISSUE=Root;  
 RC MEDLINE=95151812; Pubmed=7848072;  
 RA Siegal C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,  
 RT Marguardt H.;  
 RL "Characterization of ribosome-inactivating proteins isolated from  
 RT Bryonia dioica and their utility as carcinoma-reactive  
 RT immunocjugates.";  
 RL Bioconj.Chem. 5:423-429(1994).  
 CC -1- FUNCTION: Ribosome-inactivating protein of type 1, inhibits  
 CC protein synthesis in animal cells.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- PTM: Appears to undergo proteolytic cleavage in the C-terminal to  
 CC produce a shorter protein.  
 CC -1- BIOTECHNOLOGY: Especially useful as immunotoxin for  
 CC pharmacological applications as it has low toxicity in rats and  
 CC mice but is potent once inside target cells.  
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
 CC Type 1 RIP subfamily.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC DR EMBL; I24020; -; NOT\_ANNOTATED\_CDS.  
 CC DR PIR; S16491; S16491.  
 CC DR PDB; 1BRV; X-ray; Y/Z=23-270.  
 CC DR InterPro; IPR001574; RIP.  
 CC DR Pfam; PF00161; RIP; 1.  
 CC DR PRINTS; PR003966; SHIGARICIN.  
 CC DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 CC KM 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;  
 CC Multi-gene family; Plant defense; Protein synthesis inhibitor; Signal;  
 CC Toxin.  
 FT STGNAL 1 23  
 FT CHAIN 24 270  
 FT PROPEP 271 290  
 FT ACT\_SITE 183 183  
 FT ACT\_SITE 212 212  
 FT CARBOHYD 214 214  
 FT CARBOHYD 250 250  
 FT MOTAGEN 212 212  
 FT CONFLICT 61 65  
 FT STRAND 25 28  
 FT TURN 30 31

FT HELIX 34 46  
 FT TURN 47 47  
 FT STRAND 50 54  
 FT TURN 55 56  
 FT STRAND 57 60  
 FT HELIX 66 69  
 FT STRAND 70 76  
 FT TURN 78 79  
 FT STRAND 82 88  
 FT TURN 89 92  
 FT STRAND 93 99  
 FT TURN 100 101  
 FT STRAND 102 105  
 FT HELIX 109 114  
 FT TURN 115 117  
 FT TURN 120 121  
 FT STRAND 124 127  
 FT STRAND 134 141  
 FT HELIX 142 142  
 FT TURN 145 147  
 FT STRAND 150 150  
 FT HELIX 152 163  
 FT HELIX 164 165  
 FT TURN 167 186  
 FT HELIX 187 187  
 FT STRAND 188 196  
 FT STRAND 202 202  
 FT HELIX 206 213  
 FT TURN 214 214  
 FT HELIX 215 225  
 FT TURN 226 230  
 FT STRAND 231 239  
 FT TURN 241 242  
 FT STRAND 245 250  
 FT TURN 251 252  
 FT HELIX 254 257  
 FT TURN 258 259  
 FT STRAND 260 260  
 FT STRAND 263 263  
 FT HELIX 266 268  
 SQ SEQUENCE 290 AA; 31788 MW; E966CD9C031A42DB CRC64;  
 Query Match 87.7%; Score 1071; DB 1; Length 290;  
 Best Local Similarity 86.2%; Pred. No. 9,7e-80;  
 Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 DVSPRLSGATSSSYGVFISLNRKALPNERKLYDIPILRSSLPQSORVALIHLTNVADDTI 60  
 DB 24 DVSPRLSGATTSYGVFINKLRALPYERKVNIPILRSSISGSGYTLHLTNVADDTI 83  
 QY 61 SVAIDVTNYVIMGRAGDTSYFPENASATEAAKYVFKDARKVTLPYSGNYERLQTPACK 120  
 DB 84 SVAVDVTNYVIMGYLAGDVSYPFENASATEAAKFVKDARKVTLPYSGNYERLQTPACK 143  
 QY 121 IRENITPLGPAUDSATITLFPYANASASAMLTIOSTSEARKYKIEBOQIGRVKTF 180  
 DB 144 IRENITPLGPAUDSATITLYYYPASSASALVLIQSTESARKYKIEBOQIGRVKTF 203  
 QY 181 PSIAITSLSENSWALSQKQIQTASTNNGOFESPVLINANORRTITNVAGVTSNIAL 240  
 DB 204 PSIAITSLSENSWALSQKQIQTASTNNGOFESPVLIDGNORVSTINAGRVTSNIAL 263  
 QY 241 LNRNNMA 247  
 DB 264 LNRNNIA 270  
 RESULT 12  
 RIPL\_MOMCH STANDARD; PRT; 286 AA.  
 ID RIPL\_MOMCH  
 AC P16094; P24697;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 25-OCT-2004 (rel. 45, Laet annotation update)  
 DE Ribosome-inactivating protein momordin I precursor (EC 3.2.2.22) (rRNA  
 DE N-glycosidase) (Alpha-momorcharin) (Alpha-MMC).  
 OS Momordica charantia (Bitter melon) (Balsam pear).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid 1; Cucurbitales; Cucurbitaceae; Momordica.  
 NCBI\_Taxid=3673;  
 [1] \_\_\_\_\_  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Seed;  
 RC MEDLINE=91159486; PubMed=2001404; DOI=10.1016/0167-4781(91)90070-3;  
 RX Ho W.K.K., Liu S.C., Shaw P.C., Yeung H.W., Ng T.B., Chan W.Y.;  
 RA "Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating  
 RT protein.";  
 RL Biochim. Biophys. Acta 1088:311-314(1991).  
 RN [2]  
 RP SEQUENCE OF 24-38.  
 RC TISSUE=Seed;  
 RX MEDLINE=89326691; PubMed=2753596;  
 RA Montecucchi P.C., Lazzarini A.M., Barbieri L., Scirpe F., Soria M.,  
 RA Lapi D.;  
 RL "N-terminal sequence of some ribosome-inactivating proteins.";  
 RT Int. J. Pept. Protein Res. 33:263-267(1989).  
 RN [3]  
 RP SEQUENCE OF 24-70.  
 RC TISSUE=Seed;  
 RX MEDLINE=89005108; PubMed=3262509;  
 RA Casella P., Dussosoy D., Palasca A.I., Barbieri L., Guillemot J.C.,  
 RA Ferrara P., Bolognesi A., Centini P., Scirpe F.;  
 RT Trichostatin, a ribosome-inactivating protein from the seeds of  
 RT Trichostema kirilowii Maximowicz. Purification, partial  
 RT characterization and use for preparation of immunotoxins.";  
 RL Eur. J. Biochem. 176:581-588(1988).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=94356447; PubMed=8075985;  
 RA Ren J., Wang Y., Dong Y., Stuart D.I.;  
 RT "The N-glycosidase mechanism of ribosome-inactivating proteins implied  
 RT by crystal structures of alpha-momorcharin.";  
 RL Structure 2:7-16(1994).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.16 ANGSTROMS).  
 RX MEDLINE=94192822; PubMed=8143869; DOI=10.1016/0014-5793(94)80491-5;  
 RA Husain J., Tickle I.J., Wood S.P.;  
 RT "Crystal structure of momordin, a type I ribosome inactivating protein  
 RT from the seeds of Momordica charantia.";  
 RL FEBS Lett. 342:154-158(1994).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=95344383; PubMed=7619070;  
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;  
 RT "Studies on crystal structures, active-centre geometry and  
 RT dehydrating mechanism of two ribosome-inactivating proteins.";  
 RL Biochem. J. 309:285-298(1995).  
 CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -I- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
 CC Type 1 RIP subfamily.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X57682; CAA0869.1; -  
 DR PIR; S14273; RLPUGG  
 DR PDB; 1AH4; X-ray; @=24-269.  
 DR PDB; 1AHB; X-ray; @=24-269.  
 DR PDB; 1AHC; X-ray; @=24-269.

DR PDB; 1F8Q; X-ray; A=24-286.  
 DR PDB; 1MOM; X-ray; @=24-269.  
 DR PDB; 1MRG; X-ray; @=24-286.  
 DR PDB; 1MRH; X-ray; @=24-286.  
 DR PDB; 1MRI; X-ray; @=24-286.  
 DR GlycoStatedB; P16094; -  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KM 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;  
 KM plant defense; Protein synthesis inhibitor; Signal; Toxin.  
 FT SIGNAL 1 23  
 FT CHAIN 24 269  
 FT PROPEP 270 286  
 FT ACT SITE 183 183  
 FT CARBOHYD 250 250  
 FT STRAND 25 28  
 FT HELIX 34 47  
 FT STRAND 50 54  
 FT TURN 55 56  
 FT STRAND 57 60  
 FT HELIX 66 69  
 FT STRAND 70 76  
 FT TURN 78 79  
 FT STRAND 82 88  
 FT TURN 89 92  
 FT STRAND 93 99  
 FT TURN 100 101  
 FT STRAND 102 105  
 FT HELIX 109 114  
 FT TURN 115 117  
 FT TURN 120 121  
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 FT HELIX 134 141  
 FT HELIX 145 147  
 FT STRAND 150 150  
 FT HELIX 152 162  
 FT TURN 163 163  
 FT HELIX 167 186  
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 FT TURN 196 197  
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 FT HELIX 206 225  
 FT TURN 226 230  
 FT STRAND 231 238  
 FT TURN 240 241  
 FT STRAND 246 250  
 FT TURN 251 252  
 FT HELIX 254 258  
 FT TURN 259 259  
 FT STRAND 260 260  
 FT STRAND 263 263  
 FT HELIX 266 268  
 SQ SEQUENCE 286 AA; 31532 MW; E1B013ABBC216CF CRC64;  
 Query Match 65.7%; Score 802; DB 1; Length 286;  
 Best Local Similarity 65.2%; Pred. No. 1.2e-57;  
 Matches 161; Conservative 37; Mismatches 49; Indels 0; Gaps 0;  
 QY 1 DVSPRLSGATSSSYVPTISNRKALPNERKLYDPLPLSSLPDSQRYALHLITVYADPTI 60  
 DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 24 DVSPRLSGADPRSCTMFKDRLNALPFRKQYNIPLPLPSVSGARVYLMHLPNTDGKTI 83  
 QY 61 SVAIDVTNVIYMGVRAGDTSYFFNEASATEAKVYFKDAMRKVTLPSGNYERLQTAAGK 120  
 DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 84 TVAVDVTVYIMGVYADTTSYFENPAAELASQYFRARKKTLTPYSGNTERLQIAAGK 143  
 QY 121 IRENIPDLGPAIDSAITTLFFYNNANSAASALMTLQSTSEARKYFTIQOIGKRVDTFL 180  
 DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 144 PREKIPIGLPALDSASTLHLHYDSTPAAGALLVILQTTAAEARFXYEQIOERAYRDEV 203



QY 181 PSIAITSLSENSWALSKOIOIASTNNGQFSPVYLINAQNRVTITNVDAGVTSINAIL 240  
 DB 202 PSPAALSLSENSWALSKOIOIAQTNNGAFRTPVIIIDNKQFVEIKDVNSKVTTNNIKLL 261  
 QY 241 LNRNNMA 247  
 DB 262 LNKQNTA 268

Search completed: April 12, 2005, 15:13:59  
 Job time : 107.91 secs

## RESULT 15

0684J5 PRELIMINARY; PRT; 264 AA.  
 AC 0684J5;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Type I ribosome inactivating protein precursor (Fragment).  
 GN Name=rip;  
 OS Momordica charantia (Bitter melon) (Balsam pear).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Momordica.  
 OX NCBI\_TaxID=3673;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Nguyen Dinh C., Nguyen Thuy D., Le Thi Thu H., Nguyen Huy H.,  
 RA Tran Thi Phuong L., Nong Van H.;  
 RT "Expression of a gene encoding ribosome inactivating protein from  
 RT bitter melon (Momordica charantia).";  
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Nong V.;  
 RL Submitted (Jun-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
 CC EMBL; AJ748278; CAH19208.1; -.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Hydrolyase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 1 Potential.  
 FT CHAIN 2 264 type I ribosome inactivating protein.  
 SQ SEQUENCE 264 AA; 29775 MW; AD9E1175B70521AD CRC64;

Query Match 58.2%; Score 711; DB 2; Length 264;  
 Best Local Similarity 61.6%; Pred. No. 3.1e-50;  
 Matches 149; Conservative 31; Mismatches 60; Indels 2; Gaps 2;

QY 1 DVSFRLSGATSSSYGVFINLRKALPNEKLYDIPILRSSLPQSGRYALIHLTNYADETI 60  
 DB 2 DVNPFDSLSTAYAKYTFIEDPFRATLPFSKVDYDIPLLYSTISDSRRFILNLTSYAYETI 61  
 QY 61 SYAIDVTNYINGYRAGDTSYFENEASATEAAKYFKDAMRKVTLLPYSGNYERLQTAAGK 120  
 DB 62 SVAIDVTNYVAVYRTRDVSYPFKE-SPEPAVNIIRK-GTRKITTLPYTGNYENTLQTAHK 119  
 QY 121 IRENIPGLPLALDSAITTLFPYINANSASALNVLIOSTSEARAYKEIEQOIGKRVDTFL 180  
 DB 120 IRENIDLGLPALSSAITTLFPYNAQSPALVLIOQTAARAFKXIERHVAKYVATNPK 179  
 QY 181 PSIAITSLSENSWALSKOIOIASTNNGQFSPVYLINAQNRVTITNVDAGVTSINAIL 240  
 DB 180 PNLAITSLSENSWALSKOIOIAQTNNGAFRTPVIIIDNKQFVEIKDVNSKVTTNNIKLL 239  
 QY 241 LN 242  
 DB 240 LN 241

Query Match	99.5%	Score 1424	DB 11	Length 289
Best Local Similarity	99.7%	Pred. 1.2e-128		
Matches 289	Conservative	0	Mismatches 1	Indels 0
Gaps				
Qy	1	MIRFLVSLILITLFLFTTPAVEGDVSFPLSGATSSSYGVFISNRKALPNERKLYDIPPL	60	
Db	1	MIRFLVSLILITLFLFTTPAVEGDVSFPLSGATSSSYGVFISNRKALPNERKLYDIPPL	60	
Qy	61	RSSLPSGSORVALIHLTNVADETISSAIDVTNVIYINGVPAQDTSYFENEASATEAAKVPFK	120	
Db	61	RSSLPSGSORVALIHLTNVADETISSAIDVTNVIYINGVPAQDTSYFENEASATEAAKVPFK	120	
Qy	121	DAMRKOTLPYSGNYERLQTPAGKIRENIPLGIPALDSAITTLFYYNANSAASALMTLIQS	180	

Db 121 DAMRKVTLPYSGNYERLQTPAGKIRENIPGLG.PALDSAITTLFFYNNANSAASALMWLIOS 180  
QY 181 TSEAAKYKFEIOQIGKRVDTKFLPSLAITISLENSWSALSQIOIASTNNQGFESPVVLIN 240  
Db 181 TSEAAKYKFEIOQIGKRVDTKFLPSLAITISLENSWSALSQIOIASTNNQGFESPVVLIN 240  
QY 241 AONORVTITNVDAGVVTSNIALLLNRRNNMAAMDVDVPMTOSEFGCGSYAL 289  
Db 241 AONORVTITNVDAGVVTSNIALLLNRRNNMAAMDVDVPMTOSEFGCGSYAL 289  
RESULT 2  
US-10-280-679B-4  
; Sequence 4, Application US/10280679B  
; Publication No. US20030150019A1  
; GENERAL INFORMATION:  
; APPLICANT: Large Scale Biology Corporation  
; TITLE OF INVENTION: Monoparticle RNA Virus Transformation Vectors  
; FILE REFERENCE: LSBC-0109-US03  
; CURRENT APPLICATION NUMBER: US/10/280,679B  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: 09/557,941  
; PRIOR FILING DATE: 2000-04-24  
; PRIOR APPLICATION NUMBER: 08/484,341  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 07/923,692  
; PRIOR FILING DATE: 1992-07-31  
; PRIOR APPLICATION NUMBER: 07/600,244  
; PRIOR FILING DATE: 1990-10-22  
; PRIOR APPLICATION NUMBER: 07/641,617  
; PRIOR FILING DATE: 1991-01-16  
; PRIOR APPLICATION NUMBER: 07/737,899  
; PRIOR FILING DATE: 1991-07-26  
; PRIOR APPLICATION NUMBER: 07/739,143  
; PRIOR FILING DATE: 1991-08-01  
; PRIOR APPLICATION NUMBER: 07/310,881  
; PRIOR FILING DATE: 1989-02-17  
; PRIOR APPLICATION NUMBER: 07/160,766  
; PRIOR FILING DATE: 1988-02-26  
; PRIOR APPLICATION NUMBER: 07/160,771  
; PRIOR FILING DATE: 1988-02-26  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 289  
; TYPE: PR1  
; ORGANISM: Chinese cucumber protein alpha-trichosanthin  
US-10-280-679B-4  
Query Match 99.2%; Score 1420; DB 14; Length 289;  
Best Local Similarity 99.0%; Pred. No. 2.8e-128;  
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MIRFVLSTLITLTLPTTPAVEGDVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60  
Db 1 MIRFVLSTLITLTLPTTPAVEGDVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60  
QY 61 RSSLPGSORYALIH.LTNVADETSVAIDVTNVYIMGYRAGDTSYFENEASATEAKYVFK 120  
Db 61 RSSLPGSORYALIH.LTNVADETSVAIDVTNVYIMGYRAGDTSYFENEASATEAKYVFK 120  
QY 121 DAMRKVTLPYSGNYERLQTPAGKIRENIPGLG.PALDSAITTLFFYNNANSAASALMWLIOS 180  
Db 121 DAMRKVTLPYSGNYERLQTPAGKIRENIPGLG.PALDSAITTLFFYNNANSAASALMWLIOS 180  
QY 181 TSEAAKYKFEIOQIGKRVDTKFLPSLAITISLENSWSALSQIOIASTNNQGFESPVVLIN 240  
Db 181 TSEAAKYKFEIOQIGKRVDTKFLPSLAITISLENSWSALSQIOIASTNNQGFESPVVLIN 240  
QY 241 AONORVTITNVDAGVVTSNIALLLNRRNNMAAMDVDVPMTOSEFGCGSYAL 289  
Db 241 AONORVTITNVDAGVVTSNIALLLNRRNNMAAMDVDVPMTOSEFGCGSYAL 289

Db 241 AONORVTITNVDAGVVTSNIALLLNRRNNMAAMDVDVPMTOSEFGCGSYAI 289  
RESULT 3  
US-10-280-725B-4  
; Sequence 4, Application US/10280725B  
; Publication No. US20040049025A1  
; GENERAL INFORMATION:  
; APPLICANT: Large Scale Biology Corporation  
; TITLE OF INVENTION: Recombinant Viral Nucleic Acids  
; FILE REFERENCE: LSBC-0109-US02  
; CURRENT APPLICATION NUMBER: US/10/280,725B  
; PRIOR FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: 09/557,941  
; PRIOR FILING DATE: 2000-04-24  
; PRIOR APPLICATION NUMBER: 08/484,341  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 07/923,692  
; PRIOR FILING DATE: 1992-07-31  
; PRIOR APPLICATION NUMBER: 07/600,244  
; PRIOR FILING DATE: 1990-10-22  
; PRIOR APPLICATION NUMBER: 07/641,617  
; PRIOR FILING DATE: 1991-01-16  
; PRIOR APPLICATION NUMBER: 07/737,899  
; PRIOR FILING DATE: 1991-07-26  
; PRIOR APPLICATION NUMBER: 07/739,143  
; PRIOR FILING DATE: 1991-08-01  
; PRIOR APPLICATION NUMBER: 07/310,881  
; PRIOR FILING DATE: 1989-02-17  
; PRIOR APPLICATION NUMBER: 07/160,766  
; PRIOR FILING DATE: 1988-02-26  
; PRIOR APPLICATION NUMBER: 07/160,771  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 289  
; TYPE: PR1  
; ORGANISM: Chinese cucumber  
US-10-280-725B-4  
Query Match 99.2%; Score 1420; DB 15; Length 289;  
Best Local Similarity 99.0%; Pred. No. 2.8e-128;  
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MIRFVLSTLITLTLPTTPAVEGDVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60  
Db 1 MIRFVLSTLITLTLPTTPAVEGDVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60  
QY 61 RSSLPGSORYALIH.LTNVADETSVAIDVTNVYIMGYRAGDTSYFENEASATEAKYVFK 120  
Db 61 RSSLPGSORYALIH.LTNVADETSVAIDVTNVYIMGYRAGDTSYFENEASATEAKYVFK 120  
QY 121 DAMRKVTLPYSGNYERLQTPAGKIRENIPGLG.PALDSAITTLFFYNNANSAASALMWLIOS 180  
Db 121 DAMRKVTLPYSGNYERLQTPAGKIRENIPGLG.PALDSAITTLFFYNNANSAASALMWLIOS 180  
QY 181 TSEAAKYKFEIOQIGKRVDTKFLPSLAITISLENSWSALSQIOIASTNNQGFESPVVLIN 240  
Db 181 TSEAAKYKFEIOQIGKRVDTKFLPSLAITISLENSWSALSQIOIASTNNQGFESPVVLIN 240  
QY 241 AONORVTITNVDAGVVTSNIALLLNRRNNMAAMDVDVPMTOSEFGCGSYAL 289  
Db 241 AONORVTITNVDAGVVTSNIALLLNRRNNMAAMDVDVPMTOSEFGCGSYAI 289  
RESULT 4  
US-09-792-793A-39  
; Sequence 39, Application US/09792793A  
; Patent No. US20020168370A1  
; GENERAL INFORMATION:  
; APPLICANT: McDonald, John R.



APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 39  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Trichosantheus kirilowii  
US-09-792-793A-39

Query Match 85.3%; Score 1221; DB 9; Length 247;  
Best Local Similarity 100.0%; Pred. No. 3.4e-109;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALHILTNVADETI 83  
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALHILTNVADETI 60  
QY 84 SVAIDVTNYIMGRAGDTSYFFNEASATEAAKYVFDAMRKTYLTPYSGYERLQTPACK 143  
DB 61 SVAIDVTNYIMGRAGDTSYFFNEASATEAAKYVFDAMRKTYLTPYSGYERLQTPACK 120  
QY 144 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEAAKYKFEQOIGKRVDTFL 203  
DB 121 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEAAKYKFEQOIGKRVDTFL 180  
QY 204 PSIAIISLENSWSLSKQIQIASITNGQFESPVLINAOQRTITNVDAVGTSTNIAL 263  
DB 181 PSIAIISLENSWSLSKQIQIASITNGQFESPVLINAOQRTITNVDAVGTSTNIAL 240  
QY 264 LNRNNMA 270  
DB 241 LNRNNMA 247

RESULT 5  
US-10-375-209A-39  
Sequence 39, Application US/10375209A  
Publication No. US20030215421A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
FILE REFERENCE: 25020-601E  
CURRENT APPLICATION NUMBER: US/10/375,209A  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 39  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Trichosantheus kirilowii  
US-10-375-209A-39

Query Match 85.3%; Score 1221; DB 15; Length 247;  
Best Local Similarity 100.0%; Pred. No. 3.4e-109;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALHILTNVADETI 83  
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALHILTNVADETI 60  
QY 84 SVAIDVTNYIMGRAGDTSYFFNEASATEAAKYVFDAMRKTYLTPYSGYERLQTPACK 143  
DB 61 SVAIDVTNYIMGRAGDTSYFFNEASATEAAKYVFDAMRKTYLTPYSGYERLQTPACK 120  
QY 144 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEAAKYKFEQOIGKRVDTFL 203

DB 121 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEAAKYKFEQOIGKRVDTFL 180  
QY 204 PSIAIISLENSWSLSKQIQIASITNGQFESPVLINAOQRTITNVDAVGTSTNIAL 263  
DB 181 PSIAIISLENSWSLSKQIQIASITNGQFESPVLINAOQRTITNVDAVGTSTNIAL 240  
QY 264 LNRNNMA 270  
DB 241 LNRNNMA 247

RESULT 6  
US-10-127-890-6  
Sequence 6, Application US/10127890  
Publication No. US20030166196A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
Carroll, Stephen F.  
Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/127,890  
FILING DATE: 23-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70,P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-127-890-6

Query Match 84.5%; Score 1209; DB 14; Length 247;  
Best Local Similarity 99.2%; Pred. No. 4.9e-108;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALHILTNVADETI 83

DB 1 DVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPLRSSLPQSQRVALIHLTNVADETI 60  
QY 84 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVKDAMRKVTLPYSGNYERLQTAAGK 143  
DB 61 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVKDAMRKVTLPYSGNYERLQTAAGK 120  
QY 144 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARRYFIEQOIGKRVDTFL 203  
DB 121 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARRYFIEQOIGKRVDTFL 180  
QY 204 PSIAIISLNSWSALSQKQIQAISTNNGQFESPVLINQONQRTITNVDAVVTSNIAL 263  
DB 181 PSIAIISLNSWSALSQKQIQAISTNNGQFESPVLINQONQRTITNVDAVVTSNIAL 240  
QY 264 LNRNNMA 270  
DB 241 LNRNNMA 247

RESULT 7  
US-10-717-243-6  
Sequence 6, Application US/10717243  
Publication No. US20050054835A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
Carroll, Stephen F.  
Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/717,243  
FILING DATE: 18-Nov-2003  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/839,765  
FILING DATE: 15-APR-1997  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 1102US09/200-70.P3.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-717-243-6  
Query Match 84.5%; Score 1209; DB 17; Length 247;  
Best Local Similarity 99.2%; Pred. No. 4.9e-108;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 24 DVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPLRSSLPQSQRVALIHLTNVADETI 83  
DB 1 DVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPLRSSLPQSQRVALIHLTNVADETI 60  
QY 84 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVKDAMRKVTLPYSGNYERLQTAAGK 143  
DB 61 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVKDAMRKVTLPYSGNYERLQTAAGK 120  
QY 144 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARRYFIEQOIGKRVDTFL 203  
DB 121 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARRYFIEQOIGKRVDTFL 180  
QY 204 PSIAIISLNSWSALSQKQIQAISTNNGQFESPVLINQONQRTITNVDAVVTSNIAL 263  
DB 181 PSIAIISLNSWSALSQKQIQAISTNNGQFESPVLINQONQRTITNVDAVVTSNIAL 240  
QY 264 LNRNNMA 270  
DB 241 LNRNNMA 247

RESULT 8  
US-09-792-793A-34  
Sequence 34, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 34  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Bryonia dioica  
US-09-792-793A-34

Query Match 74.8%; Score 1071; DB 9; Length 247;  
Best Local Similarity 86.2%; Pred. No. 9.9e-95;  
Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;  
QY 24 DVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPLRSSLPQSQRVALIHLTNVADETI 83  
DB 1 DVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPLRSSLPQSQRVALIHLTNVADETI 60  
QY 84 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVKDAMRKVTLPYSGNYERLQTAAGK 143  
DB 61 SVAIDVTNYIMGYRAGDTSYFENEASATEAKYVKDAMRKVTLPYSGNYERLQTAAGK 120  
QY 144 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARRYFIEQOIGKRVDTFL 203  
DB 121 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARRYFIEQOIGKRVDTFL 180  
QY 204 PSIAIISLNSWSALSQKQIQAISTNNGQFESPVLINQONQRTITNVDAVVTSNIAL 263  
DB 181 PSIAIISLNSWSALSQKQIQAISTNNGQFESPVLINQONQRTITNVDAVVTSNIAL 240  
QY 264 LNRNNMA 270  
DB 241 LNRNNMA 247

## RESULT 9

US-10-375-209A-34  
Sequence 34, Application US/10375209A  
Publication No. US20030215421A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
FILE REFERENCE: 25020-601E  
CURRENT FILING DATE: 2003-02-24  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 34  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Bryonia dioica  
US-10-375-209A-34

Query Match 74.8%; Score 1071; DB 15; Length 247;  
Best Local Similarity 86.2%; Pred. No. 9.9e-95;  
Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 24 DVSEFRLSGATSSSYGVFISNLKRLPNERKLYDIPILRSLSLPGSQRYALHILTNVADDT 83  
DB 1 DVSEFRLSGATTSYGVFISNLKRLPNERKLYDIPILRSLSLPGSQRYALHILTNVADDT 60  
QY 84 SVAIDVTNYIMGYRAGDTSYFPENEASATEAAKYVFKDMARKYTLPSYGNRYERLQTPACK 143  
DB 61 SVAIDVTNYIMGYRAGDTSYFPENEASATEAAKYVFKDMARKYTLPSYGNRYERLQTPACK 120  
QY 144 IRENIPILGPAIDSAITTLFYNNANSAASALMWLIOSTSEAAKYKIEBOQIGKRVDTFL 203  
DB 121 IRENIPILGPAIDSAITTLFYNNANSAASALMWLIOSTSEAAKYKIEBOQIGKRVDTFL 180  
QY 204 PSIAITISLNSWSALSKQIOIASTNNGQFESPVLINAOQRTITNVDAVGTSTNIAL 263  
DB 181 PSIAITISLNSWSALSKQIOIASTNNGQFESPVLINAOQRTITNVDAVGTSTNIAL 240  
QY 264 LNRNNMA 270  
DB 241 LNRNNMA 247

## RESULT 10

US-10-127-890-7  
Sequence 7, Application US/10127890  
Publication No. US2003016196A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
Carroll, Stephen F.  
Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/127,890  
FILING DATE: 23-Apr-2002  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991

## ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248

## INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-127-890-7

Query Match 56.8%; Score 813.5; DB 14; Length 263;  
Best Local Similarity 63.8%; Pred. No. 7.2e-70;  
Matches 166; Conservative 38; Mismatches 55; Indels 1; Gaps 1;

QY 24 DVSEFRLSGATSSSYGVFISNLKRLPNERKLYDIPILRSLSLPGSQRYALHILTNVADDT 83  
DB 1 DVSEFRLSGADPSYGVFISNLKRLPNERKLYDIPILRSLSLPGSQRYALHILTNVADDT 60  
QY 84 SVAIDVTNYIMGYRAGDTSYFPENEASATEAAKYVFKDMARKYTLPSYGNRYERLQTPACK 143  
DB 61 SVAIDVTNYIMGYRAGDTSYFPENEASATEAAKYVFKDMARKYTLPSYGNRYERLQTPACK 120  
QY 144 IRENIPILGPAIDSAITTLFYNNANSAASALMWLIOSTSEAAKYKIEBOQIGKRVDTFL 203  
DB 121 IRENIPILGPAIDSAITTLFYNNANSAASALMWLIOSTSEAAKYKIEBOQIGKRVDTFL 180  
QY 204 PSIAITISLNSWSALSKQIOIASTNNGQFESPVLINAOQRTITNVDAVGTSTNIAL 263  
DB 181 PSIAITISLNSWSALSKQIOIASTNNGQFESPVLINAOQRTITNVDAVGTSTNIAL 240  
QY 264 LNRNNMAAMD-DVPMTOGF 282  
DB 241 LNRNNMAAMD-DVPMTOGF 260

## RESULT 11

US-10-717-243-7  
Sequence 7, Application US/10717243  
Publication No. US20050054835A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
Carroll, Stephen F.  
Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

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1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: Patent in Release #1.0, Version #1.25
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/10/717,243
8  FILING DATE: 18-Nov-2003
9  CLASSIFICATION: 530
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US/08/839,765
12 FILING DATE: 15-APR-1997
13 APPLICATION NUMBER: US 08/425,336
14 FILING DATE: 18-APR-1995
15 APPLICATION NUMBER: US 08/064,691
16 FILING DATE: 12-MAY-1993
17 APPLICATION NUMBER: US 07/988,430
18 FILING DATE: 09-DEC-1992
19 APPLICATION NUMBER: US 07/901,707
20 FILING DATE: 19-JUN-1992
21 APPLICATION NUMBER: US 07/787,567
22 FILING DATE: 04-NOV-1991
23 ATTORNEY/AGENT INFORMATION:
24 NAME: McNicholas, Janet M.
25 REGISTRATION NUMBER: 32,918
26 REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 312/707-8889
29 TELEFAX: 312/707-9155
30 TELEX: 650 388-1248
31 INFORMATION FOR SEQ ID NO: 7:
32 SEQUENCE CHARACTERISTICS:
33     LENGTH: 263 amino acids
34     TYPE: amino acid
35     TOPOLOGY: linear
36 MOLECULE TYPE: protein
37 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
38 US-10-717-243-7
39
40 Query Match      56.8%; Score 813.5; DB 17; Length 263;
41 Best Local Similarity 63.8%; Pred. No. 7.2e-70;
42 Matches 166; Conservative 38; Mismatches 55; Indels 1; Gaps 1
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44 QY 24 DVSFPLSGATSSVGVFISNLRKALPNEKLDIPILRBSLPSQSYALHLTMVADETI 83
45 DB 1 DVSFPLSGADPRSYGVFIFDLRNALPFRKRYNIPILLPSVSGAGRYLTMHLFNYGKTI 60
46 QY 84 SVAIVTVMYINGYRAGDTSYFENEAATEAAKYVFKDAMRKVTLLPYSGYVERLQTAAGK 143
47 DB 61 TVAVDVTMVIMGYLADTTSYFENEAALAEAGYVFRDARRKTLTLYSGYVERLQTAAGK 120
48 QY 144 IRENIPLGIPALDSAITTLFFYNANSAASALMWLIQSTSEAAKYKFIQDQIGKVDKTEFL 203
49 DB 121 PREKIPIGLPALDSAI STLHYDSTFAAGALLVLQTAEAARFKYIEQDIQERAVRDEV 180
50 QY 204 PSIAIISLNSWSALSKOIQIASTNNGQESFPVVLINAQNRRTITNVDAVGTSTIALI 263
51 DB 181 PSIAIISLNSWSGLSKOIQIAQGNNGNIFRTPVIVLDNKGNRQVITNVTSKVTSNIQLL 240
52 QY 264 INRNMAAMD-DVPMPTQSF 282
53 DB 241 LNRNIAEGDNGDVSTTHGF 260
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55 RESULT 12
56 US-10-127-890-5
57 Sequence 5, Application US/10127890
58 Publication No. US20030166196A1
59 GENERAL INFORMATION:
60 APPLICANT: Better, Marc D.
61 Carroll, Stephen F.
62 Studnicka, Gary M.
63 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

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? NUMBER OF SEQUENCES: 173 Proteins
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: McAndrews, Held & Malloy, Ltd.
? STREET: 500 West Madison Street, 34th floor
? CITY: Chicago
? STATE: Illinois
? COUNTRY: USA
? ZIP: 60661
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentia Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/10/127,890
? FILING DATE: 23-Apr-2002
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/646,360
? FILING DATE: 13-MAY-1996
? APPLICATION NUMBER: PCT/US94/05348
? FILING DATE: 12-MAY-1994
? APPLICATION NUMBER: US 08/064,691
? FILING DATE: 12-MAY-1993
? APPLICATION NUMBER: US 07/988,430
? FILING DATE: 09-DEC-1992
? APPLICATION NUMBER: US 07/901,707
? FILING DATE: 19-JUN-1992
? APPLICATION NUMBER: US 07/787,567
? FILING DATE: 04-NOV-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: McNicholas, Janet M.
? REGISTRATION NUMBER: 32,918
? REFERENCE/DOCKET NUMBER: 200-70.P4
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312/707-8889
? TELEFAX: 312/707-9155
? TELEX: 650 388-1248
? INFORMATION FOR SEQ ID NO: 5:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 248 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-127-890-5
Query Match 50.6%; Score 724.5; DB 14; Length 248;
Best Local Similarity 5.0%; Pred. No. 2.5e-61;
Matches 147; Conservative 49; Mismatches 50; Indels 3; Gaps 3
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Db 1 DVRFSLSGSSSTYSKFIIGDLRKLALPSNGVTYNNILTLSSASGASRYTLMTLNSYDKAI 60
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? 84 SVAILDVNVIIMGTRAGDTSYFPNEASLSTEAAKYVFKAMRKTYLPYGNTVERLOTAAKG 143
Db 61 TVADVDSOLXYIMGLVNSTSYFPNESDAKLSQYVFKGS-TIVLLPYSGNTEKKQTAAKG 119
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? 144 IRENPIGLPALDDAITLLFYFNANSASASALMVLIOSTSEARARYKFIOQIGKVDTFL 203
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? 204 PSIAIISIENS-WGALSKOIQIASTNNGQFESSPVLLINAQNQRVTTINVDAGVVTSNIAL 262
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? 263 LLN-RNMMA 270
Db 240 LLNTKQNVNA 248

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RESULT 13  
US-10-717-243-5  
; Sequence 5, Application US/10717243  
; Publication No. US20050054835A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Carroll, Stephen F.  
; Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/717,243  
; FILING DATE: 18-Nov-2003  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/839,765  
; FILING DATE: 15-APR-1997  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 248 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-717-243-5  
Query Match 50.6%; Score 724.5; DB 17; Length 248;  
Best Local Similarity 59.0%; Pred. No. 2.5e-61;  
Matches 147; Conservative 49; Mismatches 50; Indels 3; Gaps 3;  
QY 24 DVSFRIGATSSSYGVFISNLKRALPNERKLYIPILRSLSLPGSQRYALIHLTNYADETI 83  
DB 1 DVAFSLSSGSSSTYSKFIGDLKRALPSNGVYVLTLLSSASGASRYTTLMTLSNYDGKAI 60  
QY 84 SVAIDVTNYVMYRGADTSYFENEASATEAKYVFPDARKYTLPLYSNGVERLOTPAGK 143  
DB 61 TYAVADVSQLYIMKYLIVNSTSYFNEBDAKLASQYVERKGS-TYITLFSNGYELQTPAGK 119  
QY 144 IRENIPILGLPADLSAITTLTFYNNANSAASALMWLIQSTSEBAARYKFEIQIGKRVDTFL 203  
DB 120 IREKIPILGFPAADSALTTHIHYDSTAAAFVLVLTQTABASRFKTEGQIIRISKNGV 179

QY 204 PSIAIISLENS-WSALSQIOIASTNNGQFESPVVLINANORVITTNVAGVTSNIAL 262  
DB 180 PSIAIISLENSLSALSQIOIAAQTNNGTFKTPVITTDKQKRVETITNTSKVTATQIQ 239  
QY 263 LNLN-RNNMA 270  
DB 240 LNLNKONVA 248  
RESULT 14  
US-10-127-890-4  
; Sequence 4, Application US/10127890  
; Publication No. US20030166196A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Carroll, Stephen F.  
; Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; Proteins  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/127,890  
; FILING DATE: 23-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,360  
; FILING DATE: 13-MAY-1996  
; APPLICATION NUMBER: PCT/US94/05348  
; FILING DATE: 12-MAY-1994  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 200-70.P4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 263 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-127-890-4  
Query Match 49.5%; Score 709; DB 14; Length 263;  
Best Local Similarity 61.6%; Pred. No. 8.5e-60;  
Matches 149; Conservative 30; Mismatches 61; Indels 2; Gaps 2;  
QY 24 DVSFRIGATSSSYGVFISNLKRALPNERKLYIPILRSLSLPGSQRYALIHLTNYADETI 83  
DB 1 DVNFDLSTATKATYTKFIEDFRATLPFSHKYVDIPLYVTIIDSRRFLDLTSTAYERTI 60

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QY      84 SVAIDVTNVIYMGYRAGDTSYFENEASATEAKYVKDMARKVTLPGSGNYERLQTAAGK 143
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Db      61 SVAIDVTNVIYVAYRTRDVSYFFKE-SPEAVNIIFK-GTRKITLEPTGNYENLQTAARK 118
QY      144 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEARFYKEIQOIGKRVDTKL 203
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      119 IRENIDGLPALSSAITTLTFYNAQSPALVLQTTAEARFKYIERHAKYVATNFK 178
QY      204 PSLAIISENSWSALSQIOIASTNNGQESPVPVLINQNRVTITNVDAVVTSNIALL 263
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QY      264 LN 265
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Db      239 LN 240

RESULT 15
US-10-717-243-4
; Sequence 4, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
;   APPLICANT: Bectel, Marc D.
;             Carroli, Stephen F.
;             Studnika, Gary M.
;   TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                       Proteins
;   NUMBER OF SEQUENCES: 169
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;     STREET: 500 West Madison Street, 34th floor
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: USA
;     ZIP: 60661
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/717,243
;     FILING DATE: 18-Nov-2003
;     CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/839,765
;     FILING DATE: 15-APR-1997
;     APPLICATION NUMBER: US 08/425,336
;     FILING DATE: 18-APR-1995
;     APPLICATION NUMBER: US 08/064,691
;     FILING DATE: 12-MAY-1993
;     APPLICATION NUMBER: US 07/988,430
;     FILING DATE: 09-DEC-1992
;     APPLICATION NUMBER: US 07/901,707
;     FILING DATE: 19-JUN-1992
;     APPLICATION NUMBER: US 07/787,567
;     FILING DATE: 04-NOV-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: McNicholas, Janet M.
;     REGISTRATION NUMBER: 32,918
;     REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 312/707-8889
;     TELEFAX: 312/707-9155
;     TELEK: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 263 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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US-10-717-243-4
Query Match          49.5%; Score 709; DB 17; Length 263;
Best Local Similarity 61.6%; Pred. No. 8,5e-60;
Matches 149; Conservative 30; Mismatches 61; Indels 2; Gaps 2;

QY      24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGQRYALIHLYNVADETI 83
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1  DVNFDLSTATAKTYTKFIEDFRATLPSHKYVDIPLSTISDSRFLILDLTSYAYETI 60
QY      84 SVAIDVTNVIYMGYRAGDTSYFENEASATEAKYVKDMARKVTLPGSGNYERLQTAAGK 143
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 SVAIDVTNVIYVAYRTRDVSYFFKE-SPEAVNIIFK-GTRKITLEPTGNYENLQTAARK 118
QY      144 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEARFYKEIQOIGKRVDTKL 203
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      119 IRENIDGLPALSSAITTLTFYNAQSPALVLQTTAEARFKYIERHAKYVATNFK 178
QY      204 PSLAIISENSWSALSQIOIASTNNGQESPVPVLINQNRVTITNVDAVVTSNIALL 263
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Db      179 PHLAIISENSWSALSQIIFLAQNGGKFRNPVDLIKPTGERFQVTNVDSDVVKGNIKLL 238
QY      264 LN 265
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Db      239 LN 240

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 Job time : 96.4347 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 12, 2005, 14:53:56 ; Search time 130.481 Seconds  
(without alignments)  
856.626 Million cell updates/sec

Title: US-09-905-247A-1

Perfect score: 1431

Sequence: 1 MRRFLVLSLILTLFLITPA.....AAMDVPMQSRGCSYAL 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq.16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	1431	100.0	289	5 ABB07660	Abd07660 Native tr
2	1429	99.9	289	4 AAB99329	Aab99329 Trichosan
3	1420	99.2	289	2 AAR07514	Aar07514 Trichosan
4	1420	99.2	289	2 AAR25572	Aar25572 Trichosan
5	1420	99.2	289	2 AAR29272	Aar29272 Trichosan
6	1420	99.2	289	2 AAR55129	Aar55129 Alpha-tri
7	1420	99.2	289	2 AAM10468	Aam10468 Chinese c
8	1420	99.2	289	2 AAM11870	Aam11870 Chinese c
9	1420	99.2	289	2 AAY01374	Aay01374 Chinese c
10	1420	99.2	289	2 AAM84192	Aam84192 Chinese c
11	1420	99.2	289	3 AAY87791	Aay87791 Chinese c
12	1420	99.2	289	7 ADH44106	Adh44106 Chinese c
13	1420	99.2	289	8 ADQ43821	Adq43821 Chinese c
14	1417	99.0	289	2 AAR32986	Aar32986 Encodes c
15	1333	93.2	289	2 AAR07523	Aar07523 Alpha-Tri
16	1333	93.2	289	2 AAR29276	Aar29276 Ribosome
17	1328	92.8	267	2 AAM21703	Aam21703 Trichosan
18	1328	92.8	267	2 AAM25140	Aam25140 Trichosan
19	1321	85.3	247	3 AAY69048	Aay69048 Amino aci
20	1221	85.3	248	2 AAR07518	Aar07518 Synthetic
21	1221	85.3	248	2 AAR25573	Aar25573 Mature al
22	1218	85.1	247	2 AAR67359	Aar67359 Trichosan
23	1190	83.2	247	2 AAR21605	Aar21605 Antitumou
24	1171.5	81.9	290	2 AAR32481	Aar32481 Bryodin 1
25	1151	80.4	255	2 AAR74181	Aar74181 Type I ri

26	1146	80.1	246	2 AAR52636	Aar52636 Bioactive
27	1137	79.5	255	2 AAR37295	Aar37295 Plant typ
28	1137	79.5	255	2 AAR3907	Aar3907 Type I ri
29	1096.5	76.6	267	3 AAB01299	Aab01299 Wild type
30	1096.5	76.6	267	8 ADI05683	Adi05683 Bryonia d
31	1081	75.5	496	4 AAB36828	Aab36828 BDI-G28.5
32	1071	74.8	247	3 AAY69043	Aay69043 Amino aci
33	1071	74.8	248	4 AAB36824	Aab36824 Residues
34	1069.5	74.7	267	3 AAB01300	Aab01300 Altered b
35	911.5	63.7	267	8 ADI05689	Adi05689 Bryonia d
36	813.5	56.8	263	2 AAR63908	Aar63908 Type I ri
37	813.5	56.8	263	2 AAR74182	Aar74182 Type I ri
38	809.5	56.6	277	2 AAR29909	Aar29909 Prod. of
39	806.5	56.4	263	2 AAR37296	Aar37296 Plant typ
40	805	56.3	280	2 AAR07520	Aar07520 Alpha-Tri
41	805	56.3	280	2 AAR07521	Aar07521 Alpha-Tri
42	805	56.3	280	2 AAR25575	Aar25575 Ribosome
43	805	56.3	280	2 AAR25576	Aar25576 Ribosome
44	793.5	55.5	272	2 AAR07522	Aar07522 Alpha-Tri
45	793.5	55.5	272	2 AAR25577	Aar25577 Ribosome

## ALIGNMENTS

RESULT 1	ABB07660	standard; protein; 289 AA.
ID	ABB07660	
XX	ABB07660;	
AC		
XX		
DT	20-MAY-2002	(first entry)
XX		
DE	Native trichosanthin (TCS) protein sequence.	
XX		
KW	Trichosanthin; TCS; mutant; MTCS; therapeutic; cytostatic; antitumour;	
KW	anti-human immunodeficiency virus; virucide; immunostimulant; gene;	
KW	ectopic pregnancy.	
XX		
OS	Trichosanthes kirilowii.	
XX		
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..23
FT	Misc-difference	/note= "signal peptide"
FT	Protein	24..289
FT		/note= "mature protein"
FT	Region	174..180
FT		/note= "MTCS contains a modification of at least one amino acid residue in this region"
FT	Misc-difference	175
FT		/note= "encoded by ATT"
FT	Region	203..226
FT		/note= "MTCS contains a modification of at least one amino acid residue in this region"
FT	Region	230..244
FT		/note= "MTCS contains a modification of at least one amino acid residue in this region"
FT	Misc-difference	289
FT		/note= "encode dby ATT"
PN	WO200212537-A2.	
XX		
PD	14-FEB-2002.	
XX		
PF	18-JUL-2001; 2001MO-CN001178.	
XX		
PR	02-AUG-2000; 2000CN-00119553.	
XX		
PR	18-JAN-2001; 2001CN-00103102.	
XX		
PA	(BEIJ- ) BEIJING STM BIOTECH LTD.	
PA	(KEYV/) KE Y.	

PA (NIEH/) NIE H.  
 XX  
 XX Ke Y, Nie H;  
 XX  
 DR MPI; 2002-227165/28.  
 DR N-PSDB; ABA95171.  
 XX  
 XX Mutant trichosanthin protein of low antigenicity useful for treating  
 PT tumor e.g. leukemia, comprises a sequence of native trichosanthin with  
 PT modification of at least one amino acid residue in three specific  
 PT regions.  
 XX  
 PS Example 1; Fig 1; 42pp; English.  
 XX  
 CC The invention relates to a mutant trichosanthin (MTCS) protein of low  
 CC antigenicity comprising a sequence of native TCS with the modification of  
 CC at least one amino acid residue in three regions which is 174-180, 203-  
 CC 227 and 230-244 and substantially retaining the biological activities of  
 CC the native TCS. The MTCS protein, its fragment or derivative is useful as  
 CC an therapeutic agent; or for preparing a medicament for treating viral  
 CC disease e.g. acquired immunodeficiency syndrome (AIDS), tumour e.g. 'the  
 CC leukemia, for inducing abortion and/or treating ectopic pregnancy. The  
 CC present sequence represents the native TCS  
 XX  
 SQ Sequence 289 AA;

Query Match 100.0%; Score 1431; DB 5; Length 289;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-127;  
 Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFVLVSLILITLFLTPAVGDSFRLSGATSSSYGVFISNLKALPNERKLDIPLL 60  
 DB 1 MRFVLVSLILITLFLTPAVGDSFRLSGATSSSYGVFISNLKALPNERKLDIPLL 60  
 QY 61 RSLPSQRYALIHNTYADETISVAIDVTNYIMGRAGDTSYFNEASATEAAKYVK 120  
 DB 61 RSLPSQRYALIHNTYADETISVAIDVTNYIMGRAGDTSYFNEASATEAAKYVK 120  
 QY 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSAITTLFYNNANSAASALMWLIQS 180  
 DB 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSAITTLFYNNANSAASALMWLIQS 180  
 QY 181 TSEARXYKEIEQIGKRVDTPLPSLAISLENSWSALSQIQIASTNNGQFESPVLIN 240  
 DB 181 TSEARXYKEIEQIGKRVDTPLPSLAISLENSWSALSQIQIASTNNGQFESPVLIN 240  
 QY 241 AONORVTITNDAGVVTNSIALILNRNNMAAMDDVPMTQSFQCGSYAL 289  
 DB 241 AONORVTITNDAGVVTNSIALILNRNNMAAMDDVPMTQSFQCGSYAL 289

RESULT 2  
 AAB99329  
 ID AAB99329 standard; protein; 289 AA.  
 XX  
 AC AAB99329;  
 XX  
 DT 23-AUG-2001 (first entry)  
 XX

DE Trichosanthes kirilowii trichosanthin (TCS) protein sequence.  
 XX  
 KW Trichosanthes kirilowii; trichosanthin; TCS; mutagenesis; mutation; MTCS;  
 KM mutant of trichosanthin; Mongolian snake-gourd; bioactivity; selectivity;  
 KM cancer; virus; HIV; metaphase induced labour.

OS Trichosanthes kirilowii.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 230  
 FT /note= "encoded by GCA"  
 XX  
 XX CN1283630-A.  
 XX

PD 14-FEB-2001.  
 XX  
 PF 02-AUG-2000; 2000CN-00119553.  
 XX  
 XX 02-AUG-2000; 2000CN-00119553.  
 XX  
 XX (SHAN-) SHANGHAI INST CYTOBIOLOGY CHINESE ACAD.  
 PA  
 XX Ke Y, Nie H;  
 XX  
 PI MPI; 2001-291745/31.  
 XX  
 DR N-PSDB; AAR41473.  
 XX  
 XX Trichosanthin mutant and its preparing process.  
 PT  
 PS Disclosure; Page 2 (disclosure); 15pp; Chinese.  
 XX  
 CC The present invention describes a trichosanthin mutant which is prepared  
 CC through the mutational deformation of the trichosanthin gene and using an  
 CC expression system. The trichosanthin gene is isolated from Trichosanthes  
 CC kirilowii (Mongolian snake-gourd). The trichosanthin mutant has several  
 CC advantages including high bioactivity, high selectivity to target, and  
 CC strong kill action to cancer cells, virus and HIV. It can also be used  
 CC for metaphase induced labour. The present sequence represents the protein  
 CC sequence of wild type trichosanthin which is given in the exemplification  
 CC of the present invention  
 XX  
 SQ Sequence 289 AA;

Query Match 99.9%; Score 1429; DB 4; Length 289;  
 Best Local Similarity 99.7%; Pred. No. 1.7e-127;  
 Matches 288; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFVLVSLILITLFLTPAVGDSFRLSGATSSSYGVFISNLKALPNERKLDIPLL 60  
 DB 1 MRFVLVSLILITLFLTPAVGDSFRLSGATSSSYGVFISNLKALPNERKLDIPLL 60  
 QY 61 RSLPSQRYALIHNTYADETISVAIDVTNYIMGRAGDTSYFNEASATEAAKYVK 120  
 DB 61 RSLPSQRYALIHNTYADETISVAIDVTNYIMGRAGDTSYFNEASATEAAKYVK 120  
 QY 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSAITTLFYNNANSAASALMWLIQS 180  
 DB 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSAITTLFYNNANSAASALMWLIQS 180  
 QY 181 TSEARXYKEIEQIGKRVDTPLPSLAISLENSWSALSQIQIASTNNGQFESPVLIN 240  
 DB 181 TSEARXYKEIEQIGKRVDTPLPSLAISLENSWSALSQIQIASTNNGQFESPVLIN 240  
 QY 241 AONORVTITNDAGVVTNSIALILNRNNMAAMDDVPMTQSFQCGSYAL 289  
 DB 241 AONORVTITNDAGVVTNSIALILNRNNMAAMDDVPMTQSFQCGSYAL 289

RESULT 3  
 AAR07514  
 ID AAR07514 standard; protein; 289 AA.  
 XX  
 AC AAR07514;  
 XX  
 DT 06-FEB-1991 (first entry)  
 XX

DE Trichosanthin from Trichosanthes kirilowii.  
 XX  
 KW trichosanthin (TCS); Human Immunodeficiency Virus; inhibition.  
 KM trichosanthin (TCS); Human Immunodeficiency Virus; inhibition.

OS Trichosanthes kirilowii.  
 XX  
 FH Key Location/Qualifiers  
 FT 1.21  
 FT Region  
 FT /label= "signal peptide"  
 FT /note= "hydrophobic"  
 XX



PN WO9012097-A.  
 XX  
 PD 18-OCT-1990.  
 XX  
 PF 04-APR-1989; 89US-00333184.  
 XX  
 PR 04-APR-1989; 89US-00333184.  
 XX  
 PA (GENE-) GENELABS INC.  
 XX  
 PI Platek M, Chow T, Fry K;  
 XX  
 DR MPI; 1990-334847/44.  
 XX  
 DR N-PSDB; AAQ06343.  
 XX  
 PT Recombinant tri:chosanthin protein - with selective inhibitory effect on  
 PT viral expression in HIV infected T-cells or monocyte-macrophase.  
 XX  
 PS Example; Fig 4; 102pp; English.  
 XX  
 CC Genomic DNA was isolated from T.kirilowi leaves from Korea and a library  
 CC was constructed. Clone pQ21D was identified as likely to contain a TCS-  
 CC encoding sequence in its 4kb insert. The deduced amino acid sequence is  
 CC identical to that of TCS purified from Cantonese T.kirilowi roots,  
 CC except for 2 conservative substitutions, i.e. Thr for Ser at position  
 CC 211 and Met for Thr at position 224. The Canton protein lacks the last 19  
 CC C-terminal amino acid residues. See also AAQ06344-Q06351  
 XX  
 SQ Sequence 289 AA;  
 XX  
 Query Match 99.2%; Score 1420; DB 2; Length 289;  
 Best Local Similarity 99.0%; Pred. No.1.2e-126;  
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRFVLVSLILTLFTTPAVEGDVSPRLSGATSSSYGVFISMLRKALPNERKLYDIPLL 60  
 DB 1 MRFVLVSLILTLFTTPAVEGDVSPRLSGATSSSYGVFISMLRKALPNERKLYDIPLL 60  
 QY 61 RSLPSSORYALHLNNYADETISVAIDVTNVTINGRAGDTSYFFNEASATAKYYVK 120  
 DB 61 RSLPSSORYALHLNNYADETISVAIDVTNVTINGRAGDTSYFFNEASATAKYYVK 120  
 QY 121 DAARKVTLPYSGYERLQTPAGKIRENIPGLPALDSATTLFYYNANSAASLMTLLOS 180  
 DB 121 DAARKVTLPYSGYERLQTPAGKIRENIPGLPALDSATTLFYYNANSAASLMTLLOS 180  
 QY 181 TSEAAKYKFEQIGRVDKTFPLSLAISLENSWSALSKQIOIASTNNQGFPPVVLIN 240  
 DB 181 TSEAAKYKFEQIGRVDKTFPLSLAISLENSWSALSKQIOIASTNNQGFPPVVLIN 240  
 QY 241 AONQRTTINVDAGVTSNIALILNRRNNMAAMDVDVPMQTGFCGSGYAL 289  
 DB 241 AONQRTTINVDAGVTSNIALILNRRNNMAAMDVDVPMQTGFCGSGYAL 289

RESULT 4  
 AAR25572  
 ID AAR25572 standard; protein; 289 AA.  
 XX  
 AC AAR25572;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 13-JAN-1993 (first entry)  
 XX  
 DE Trichosanthin from Trichosanthes kirilowii.  
 KM TCS: alpha-trichosanthin; Radix trichosanthin; abortifacient;  
 KM ribosome inactivating protein; RIP; HIV-infected human T cells;  
 KM human immunodeficiency virus.  
 OS Trichosanthes kirilowii.  
 OS  
 FH Key Location/Qualifiers

FT Misc-difference 57 /note= "Leu in previously published sequence"  
 FT FT  
 FT Misc-difference 60 /note= "Ile in previously published sequence"  
 FT FT  
 FT Misc-difference 72 /note= "Ile in previously published sequence"  
 FT FT  
 FT Misc-difference 82.84 /note= "region not present in previously published  
 FT sequence"  
 FT FT  
 FT Misc-difference 92.93 /note= "previously published sequence contained a 10  
 FT amino acid insert (DAGLPRNNAV) between Val and Tyr"  
 FT FT  
 FT Misc-difference 143 /note= "Gly in previously published sequence"  
 FT FT  
 FT Misc-difference 144 /note= "Leu in previously published sequence"  
 FT FT  
 FT Misc-difference 196 /note= "Ser in previously published sequence"  
 FT FT  
 FT Misc-difference 214.225 /note= "previously published sequence contained a Leu  
 FT inserted between Ser and Trp"  
 FT FT  
 FT Misc-difference 216 /note= "Leu in previously published sequence"  
 FT FT  
 FT Misc-difference 231 /note= "Thr in previously published sequence"  
 FT FT  
 FT Misc-difference 234 /note= "Ser in directly sequenced TCS"  
 FT FT  
 FT Misc-difference 246.266 /note= "21 amino acids not present in previously  
 FT published sequence"  
 FT FT  
 FT Misc-difference 247 /note= "Thr in directly sequenced TCS"  
 FT FT

PN US5128460-A.  
 XX  
 PD 07-JUL-1992.  
 XX  
 PF 04-APR-1990; 90US-00504775.  
 XX  
 PR 04-APR-1989; 89US-00333184.  
 PR 07-SEP-1989; 89US-00404326.  
 XX  
 PA (GENE-) GENELABS INC.  
 XX  
 PI Platek M, Chow TP, Fry K;  
 XX  
 DR MPI; 1992-249485/30.  
 DR N-PSDB; AAQ26499.  
 XX  
 PT Nucleic acid encoding trichosanthin protein - which can be used to  
 PT inactivate ribosome(s) to inhibit protein synthesis or to inhibit HIV  
 PT expression.  
 XX  
 PS Claim 1; Fig 4; 53pp; English.

Trichosanthin protein was isolated from T.kirilowi root tuber and  
 CC sequenced. The amino acid sequence was used to design sets of degenerate  
 CC primers (see AAQ26506-8) for PCR amplification of the TCS coding  
 CC sequence. The amplified product was used as a probe to isolate TCS coding  
 CC sequence from T.kirilowi genomic libraries. One clone (pQ21D) contained  
 CC a 4kb insert. The amino acid sequence deduced from the pQ21D insert  
 CC differed from the purified TCS sequence by conservative substitutions at  
 CC two positions (see Features Table). The differences are postulated to  
 CC indicate minor variations between strains; the purified TCS was obtained  
 CC from the Canton region of China and the genomic DNA was obtained from  
 CC T.kirilowi leaves from Korea. The amino acid sequence was also found to  
 CC differ substantially from the previously published TCS sequence (Acta  
 CC Chemica Sinica, 43:943, 1984 and Pure and Appl. Chem., 58(5):789, 1986).  
 CC The differences are shown in the Features Table. The present sequence  
 CC agrees closely with X-ray diffraction data on crystallized TCS. The 21-  
 CC amino acid insert also provides greater sequence homology with a number  
 CC of RIPs such as ricin A chain and abrin A chain than the previously  
 CC published sequence. (Updated on 25-MAR-2003 to correct PF field.)

CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 2; Length 289;

Best Local Similarity 99.0%; Pred. No. 1.2e-126; Mismatches 1; Indels 0; Gaps 0;

Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVLSLLIITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60  
DB 1 MIRFLVLSLLIITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60  
QY 61 RSSLPGSQRYALIHLTNVADETSVAIDVTNVIYMGVYAGDTSYFENEASATEAKYVK 120  
DB 61 RSSLPGSQRYALIHLTNVADETSVAIDVTNVIYMGVYAGDTSYFENEASATEAKYVK 120  
QY 121 DAMRKVTLPYSGNYERLQTPAAGKIRENIPGLPALDSAITTLFYNNASASALMWLIQS 180  
DB 121 DAMRKVTLPYSGNYERLQTPAAGKIRENIPGLPALDSAITTLFYNNASASALMWLIQS 180  
QY 181 TSEARVYKFEIOQIGKRVDTFLPSLAISLENSWSALSQIOIASTNNGOFETPVVLIN 240  
DB 181 TSEARVYKFEIOQIGKRVDTFLPSLAISLENSWSALSQIOIASTNNGOFETPVVLIN 240  
QY 241 AONORVTITNDAGVVTNSIALILNRMNMAAMDDVPMTOQSFQCGSYAI 289  
DB 241 AONORVTITNDAGVVTNSIALILNRMNMAAMDDVPMTOQSFQCGSYAI 289

#### RESULT 5

AAR29272 standard; protein; 289 AA.

XX AAR29272;

DT 25-MAR-2003 (revised)

DT 16-APR-1993 (first entry)

DE Trichosanthin protein (encoded by pQ21D).

KW TCS; alpha-trichosanthin; Radix-trichosanthin; primer; inhibition;

XX viral expression; HIV; T-cell; macrophage.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..23

FT Protein /label= sig\_peptide

FT Protein /note= "putative N-terminal extension of the mature TCS"

FT Misc-difference 234

FT Misc-difference 247

FT Protein /note= "plant-derived TCS has Ser at this position"

FT Protein /note= "putative C-terminal extension of the mature TCS"

XX US516056-A.

XX 24-NOV-1992.

XX 09-DEC-1991; 91US-00804293.

XX 04-APR-1989; 89US-0033184.

XX 07-SEP-1989; 89US-00404326.

XX (GENE-) GENELABS INC.

XX Piatek M, Chow TP;

XX WPI; 1992-414954/50.

PT Recombinant Trichosanthin protein prodn. in E. coli - for use in the  
XX selective inhibition of viral expression in HIV infected cells.

XX Disclosure; Fig 4; 37pp; English.

CC The sequence is identical to that of plant-derived TCS except for two  
CC conservative changes: a Thr for a Ser substitution at position 211 and a  
CC Met for a Thr substitution at position 224. TCS is likely produced as a  
CC secreted protein that undergoes post-translational processing at both the  
CC amino and carboxy ends. The TCS coding sequence was amplified using the  
CC primers of AAQ31828-30. The amplified prod. has the sequence of AAQ31827,  
CC which was used as a probe. One isolate, pQ21D, comprises the sequence of  
CC AAQ31826. The recombinant TCS sequence may be used in the recombinant  
CC prodn. of TCS. TCS can be used for the selective inhibition of viral  
CC expression in HIV-infected human T-cells or macrophages. (Updated on 25-  
CC MAR-2003 to correct PF field.)

XX Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 2; Length 289;

Best Local Similarity 99.0%; Pred. No. 1.2e-126; Mismatches 1; Indels 0; Gaps 0;

Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVLSLLIITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60  
DB 1 MIRFLVLSLLIITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60  
QY 61 RSSLPGSQRYALIHLTNVADETSVAIDVTNVIYMGVYAGDTSYFENEASATEAKYVK 120  
DB 61 RSSLPGSQRYALIHLTNVADETSVAIDVTNVIYMGVYAGDTSYFENEASATEAKYVK 120  
QY 121 DAMRKVTLPYSGNYERLQTPAAGKIRENIPGLPALDSAITTLFYNNASASALMWLIQS 180  
DB 121 DAMRKVTLPYSGNYERLQTPAAGKIRENIPGLPALDSAITTLFYNNASASALMWLIQS 180  
QY 181 TSEARVYKFEIOQIGKRVDTFLPSLAISLENSWSALSQIOIASTNNGOFETPVVLIN 240  
DB 181 TSEARVYKFEIOQIGKRVDTFLPSLAISLENSWSALSQIOIASTNNGOFETPVVLIN 240  
QY 241 AONORVTITNDAGVVTNSIALILNRMNMAAMDDVPMTOQSFQCGSYAI 289  
DB 241 AONORVTITNDAGVVTNSIALILNRMNMAAMDDVPMTOQSFQCGSYAI 289

#### RESULT 6

AAR55129 standard; protein; 289 AA.

XX AAR55129;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 11-JAN-1995 (first entry)

DE Alpha-trichosanthin coding.

KW Virus; recombination; plant virus; alpha trichosanthin; phenotype;

XX alpha amylase; alpha haemoglobin; brome mosaic virus; gemini virus;

XX rice necrosis virus tobamovirus; gene expression; chinese cucumber.

XX Trichosanthin Kirilowii.

XX US5316931-A.

XX 31-MAY-1994.

XX 31-JUL-1992; 92US-00923692.

XX 26-FEB-1988; 88US-00160766.

XX 15-JUL-1988; 88US-00219279.

XX 17-FEB-1989; 89US-00310881.

XX 05-MAY-1989; 89US-00347637.

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PR 08-JUN-1989; 89US-00363138.
PR 22-OCT-1990; 90US-00600244.
PR 16-JAN-1991; 91US-00641617.
PR 26-JUL-1991; 91US-00737899.
PR 01-AUG-1991; 91US-00739143.
XX
XX (BIOS-) BIOSOURCE GENETICS CORP.
XX
XX Garger SJ, Turpen AM, Grill LK, Grantham GL, Dawson WO, Denson J,
PI Turpen TH;
XX
XX WPI; 1994-176269/21.
XX N-PSDB; AAQ65573.
XX
XX New recombinant plant viral nucleic acid - capable of systemic infection
PT and stable expression of non-native nucleic acid in plant host.
XX
XX Example 4; Col 47-50; 44pp; English.
XX
XX The alpha-trichosanthin gene may be inserted into a recombinant plant
CC virus which can then be used to infect plants for the production of non-
CC native products (in this case alpha-trichosanthin). Other genes which
CC may be inserted into the virus are those which control a phenotypic
CC trait, such as male sterility, or sequences encoding anti-sense RNA which
CC can be useful to prevent the expression of undesired phenotypic traits.
CC The recombinant virus is derived from a plus sense, single stranded virus
CC selected from tobamovirus, bromo mosaic virus, rice necrosis virus or a
CC gemini virus. (Updated on 25-MAR-2003 to correct PF field.) (Updated on
CC 27-AUG-2003 to correct OS field.)
XX
XX Sequence 289 AA;
SQ
Query Match 99.2%; Score 1420; DB 2; Length 289;
Best Local Similarity 99.0%; Pred. No. 1.2e-126;
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIRFLVSLILILFLTPPAVEGVSPRLSGATSSSYGVFISMLRKALPNERKLYDIPLL 60
DB 1 MIRFLVSLILILFLTPPAVEGVSPRLSGATSSSYGVFISMLRKALPNERKLYDIPLL 60
QY 61 RSSLPQSQRVALHLTNVADETTISVAIDVTNVYIMGRAGDTSYFFNEASATEAAKYVF 120
DB 61 RSSLPQSQRVALHLTNVADETTISVAIDVTNVYIMGRAGDTSYFFNEASATEAAKYVF 120
QY 121 DAMRKVTLPYSGYVERLQTAAGKIRENIPGLPALDSAITTLFYYNANSASALMVLIO 180
DB 121 DAMRKVTLPYSGYVERLQTAAGKIRENIPGLPALDSAITTLFYYNANSASALMVLIO 180
QY 181 TSEAAKYKFEQOIGKRVDTFLPSLAITISLENSWSLSKOIOIATNNQFESPVLIN 240
DB 181 TSEAAKYKFEQOIGKRVDTFLPSLAITISLENSWSLSKOIOIATNNQFESPVLIN 240
QY 241 AQORVITINVDAGVVTSNIALLLNRNNMAAMDDVPMTOSFGCGSYAL 289
DB 241 AQORVITINVDAGVVTSNIALLLNRNNMAAMDDVPMTOSFGCGSYAI 289
RESULT 7
AAW10468
ID AAW10468 standard; protein; 289 AA.
XX
XX AAW10468;
XX
XX 17-OCT-2003 (revised)
DT 26-APR-1997 (first entry)
XX
XX Chinese cucumber alpha-trichosanthin.
DE
XX
XX Recombinant viral nucleic acid; RNA virus; vector; tobacco mosaic virus;
KM TWV; Chinese cucumber; alpha-trichosanthin;
KM ribosome inactivating protein; antiviral; virucide; transgenic plant.
OS
XX Trichosanthes kirilowii; Maximowicz.

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XX
XX WO640867-A1.
PN
XX 19-DEC-1996.
PD
XX
XX 06-JUN-1996; 96WO-US009299.
XX
XX 07-JUN-1995; 95US-00483502.
XX
XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.
XX
XX Denson J, Dawson WO, Grantham GL, Turpen TH, Turpen AM;
PI Garger SJ, Grill LK;
XX
XX WPI; 1997-065181/06.
XX N-PSDB; AAT47094.
XX
XX Recombinant viral nucleic acid producing, e.g. male sterility in plants -
PT comprises nucleic acid whose transcription is controlled by another
PT sequence.
XX
XX Example 4; Page 124-125; 149pp; English.
XX
XX Chinese cucumber alpha-trichosanthin (AAW10468) is a ribosome
CC inactivating protein of potential use in the treatment of HIV infection.
CC Expression vector pBC152 was constructed in which the alpha-
CC trichosanthin coding sequence (see also AAT47094) was placed under
CC control of the promoter of the tobacco mosaic virus-U1 coat protein gene,
CC which had been deleted. The viral nucleic acid was capable of self-
CC replication, encapsidation and systemic spread in infected Nicotiana
CC benthamiana plants, and directed the high-level expression of
CC biologically active alpha-trichosanthin in plant tissues. (Updated on 17-
CC OCT-2003 to standardise OS field)
XX
XX Sequence 289 AA;
SQ
Query Match 99.2%; Score 1420; DB 2; Length 289;
Best Local Similarity 99.0%; Pred. No. 1.2e-126;
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIRFLVSLILILFLTPPAVEGVSPRLSGATSSSYGVFISMLRKALPNERKLYDIPLL 60
DB 1 MIRFLVSLILILFLTPPAVEGVSPRLSGATSSSYGVFISMLRKALPNERKLYDIPLL 60
QY 61 RSSLPQSQRVALHLTNVADETTISVAIDVTNVYIMGRAGDTSYFFNEASATEAAKYVF 120
DB 61 RSSLPQSQRVALHLTNVADETTISVAIDVTNVYIMGRAGDTSYFFNEASATEAAKYVF 120
QY 121 DAMRKVTLPYSGYVERLQTAAGKIRENIPGLPALDSAITTLFYYNANSASALMVLIO 180
DB 121 DAMRKVTLPYSGYVERLQTAAGKIRENIPGLPALDSAITTLFYYNANSASALMVLIO 180
QY 181 TSEAAKYKFEQOIGKRVDTFLPSLAITISLENSWSLSKOIOIATNNQFESPVLIN 240
DB 181 TSEAAKYKFEQOIGKRVDTFLPSLAITISLENSWSLSKOIOIATNNQFESPVLIN 240
QY 241 AQORVITINVDAGVVTSNIALLLNRNNMAAMDDVPMTOSFGCGSYAL 289
DB 241 AQORVITINVDAGVVTSNIALLLNRNNMAAMDDVPMTOSFGCGSYAI 289
RESULT 8
AAW11870
ID AAW11870 standard; protein; 289 AA.
XX
XX AAW11870;
XX
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-APR-1997 (first entry)
XX
XX Chinese cucumber alpha-trichosanthin.
DE
XX

```

KM Recombinant virus; alpha-haemoglobin; human; chinese cucumber;  
 KM alpha-trichosanthin; rice; alpha amylase; beta-haemoglobin;  
 XX subgenomic promoter; coat protein.  
 OS Cucumis sp.  
 XX  
 PN US589367-A.  
 XX  
 PD 31-DEC-1996.  
 XX  
 PF 19-JAN-1994; 94US-00184237.  
 XX  
 PR 26-FEB-1988; 88US-00160766.  
 PR 26-FEB-1988; 88US-00160771.  
 PR 15-JUL-1988; 88US-00219279.  
 PR 17-FEB-1989; 89US-00310881.  
 PR 05-MAY-1989; 89US-00347637.  
 PR 08-JUN-1989; 89US-00363138.  
 PR 22-OCT-1990; 90US-00600244.  
 PR 16-JAN-1991; 91US-00641617.  
 PR 26-JUL-1991; 91US-00737899.  
 PR 01-AUG-1991; 91US-00739143.  
 PR 31-JUL-1992; 92US-00923692.  
 XX  
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.  
 XX  
 PI Garger SJ, Turpen AM, Grill LK, Grantham GL, Donson J, Dawson WO;  
 PI Turpen TH;  
 XX  
 DR WPI: 1997-076845/07.  
 XX  
 N-PSDB; AAT61376.  
 XX  
 PT Recombinant viral DNA for altering plant phenotype or protein prodn -  
 PT contains non-native sub-genomic promoter for expression of heterologous  
 PT protein and native promoter for expression of coat protein.  
 XX  
 PS Example 4; Col 45-46; 42bp; English.  
 XX  
 XX The sequences given in AAM1868-71 represent proteins which were produced  
 CC by the recombinant viruses of the invention. The viruses are recombinant  
 CC plant viruses which comprise a native plant virus subgenomic promoter, at  
 CC least one non-native plant virus subgenomic promoter, and a sequence  
 CC encoding a plant virus coat protein. These heterologous sequences are  
 CC preferably under the control of the native promoter sequence. By using a  
 CC plant virus existing cells can be altered with a new coding sequence  
 CC without involving germ cell. The recombinant viruses are stable and can  
 CC cause systemic infection, with stable expression/transcription in plants  
 CC that are hosts for the non-native part of the vector. The nucleotide  
 CC sequences encoding these protein preferably integrated in plant viruses  
 CC having either the O-coat protein or the UI-coat protein gene. (Updated on  
 CC 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR  
 CC field.) (Updated on 27-AUG-2003 to correct OS field.)  
 CC  
 SO Sequence 289 AA;  
 Query Match 99.2%; Score 1420; DB 2; Length 289;  
 Best Local Similarity 99.0%; Pred. No. 1,2e-126;  
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 181 TSEAAKYKIEQIGKRVKTFPLSLAITSLENSWSALSKOIQIASTNNGFETPVILIN 240  
 QY 241 AONORVTITNDAGVVTSTNIALLRNNMAAMDVPMTQSFCCSYAL 289  
 |||||  
 DB 241 AONORVMITNDAGVVTSTNIALLRNNMAAMDVPMTQSFCCSYAL 289  
 RESULT 9  
 AAY01374  
 ID AAY01374 standard; protein; 289 AA.  
 XX  
 AC AAY01374;  
 XX  
 DT 20-MAR-2003 (revised)  
 DT 04-JUN-1999 (first entry)  
 XX  
 DE Chinese cucumber alpha-trichosanthin.  
 XX  
 KM Recombinant; plant virus; coat protein; systemic infection;  
 KM transcription; therapeutic; chinese cucumber; alpha-trichosanthin.  
 XX  
 OS Cucumis sp.  
 XX  
 PN US5893190-A.  
 XX  
 PD 30-MAR-1999.  
 XX  
 PF 07-JUN-1995; 95US-00480432.  
 XX  
 PR 26-FEB-1988; 88US-00160766.  
 PR 26-FEB-1988; 88US-00160771.  
 PR 15-JUL-1988; 88US-00219279.  
 PR 17-FEB-1989; 89US-00310881.  
 PR 05-MAY-1989; 89US-00347637.  
 PR 08-JUN-1989; 89US-00363138.  
 PR 22-OCT-1990; 90US-00600244.  
 PR 16-JAN-1991; 91US-00641617.  
 PR 26-JUL-1991; 91US-00737899.  
 PR 01-AUG-1991; 91US-00739143.  
 PR 31-JUL-1992; 92US-00923692.  
 PR 19-JAN-1994; 94US-00184237.  
 XX  
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.  
 XX  
 PI Garger SJ, Turpen AM, Grill LK, Grantham GL, Donson J, Dawson WO;  
 PI Turpen TH;  
 XX  
 DR WPI: 1999-243290/20.  
 XX  
 N-PSDB; AAX29143.  
 XX  
 PT Recombinant plant viral nucleic acid derived from a plus sense, single  
 PT stranded RNA plant virus - useful for the transcription of products in a  
 PT host.  
 XX  
 PS Example 4; Col 43-46; 46bp; English.  
 XX  
 XX The invention relates to a recombinant plant viral nucleic acid derived  
 CC from a plus sense, single stranded RNA plant virus. The recombinant plant  
 CC viral nucleic acid comprises: (a) a first plant viral subgenomic promoter  
 CC that is native to the plus sense, single stranded RNA plant virus and  
 CC operably joined to a first nucleic acid expression sequence; and (b) a  
 CC second plant viral subgenomic promoter that is non-native and is operably  
 CC joined to a second nucleic acid expression sequence; where, (i) (a) and  
 CC (b) are incapable of recombination with one another, (ii) either the  
 CC first or the second nucleic acid expression sequence is a plant viral  
 CC coat protein coding sequence. The recombinant plant viral nucleic acid  
 CC allows the transcription of products in a host, such as therapeutic and  
 CC other useful polypeptides or proteins e.g. enzymes, complex biomolecules  
 CC and ribozymes. It also gives the option of applying the coding sequence  
 CC to the desired organism, tissue, organ or cell, is stable for the foreign  
 CC coding sequences and is capable of systemic infection in the plant host.  
 CC The transformation and regeneration of target organisms become  
 CC unnecessary. (Updated on 20-MAR-2003 to correct PR field.)

XX Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 2; Length 289;  
Best Local Similarity 99.0%; Pred. No. 1.2e-126;  
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVSLILILFLTPAVEGVDFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60  
DB 1 MIRFLVSLILILFLTPAVEGVDFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60  
QY 61 RSSLPQSORVALIHLTNVADETISVALDVNTVYIMGYRADTSYFNEASATEAAKYVFK 120  
DB 61 RSSLPQSORVALIHLTNVADETISVALDVNTVYIMGYRADTSYFNEASATEAAKYVFK 120  
QY 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSATITLFFYNNASAAALMVLIO 180  
DB 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSATITLFFYNNASAAALMVLIO 180  
QY 181 TSEARARYKTEQOIGKRVDTFLPSLAITSLNSWSLSKOIOIATSTNNGQFETPVVLIN 240  
DB 181 TSEARARYKTEQOIGKRVDTFLPSLAITSLNSWSLSKOIOIATSTNNGQFETPVVLIN 240  
QY 241 AQORVITINVDAGVVTSNIALILNRNNMAAMDVDVPMTOSFGCGSYAI 289  
DB 241 AQORVITINVDAGVVTSNIALILNRNNMAAMDVDVPMTOSFGCGSYAI 289

## RESULT 10

AAW84192  
ID AAW84192 standard; protein; 289 AA.

AC AAW84192;

DT 27-AUG-2003 (revised)  
DT 01-APR-1999 (first entry)

XX Chinese cucumber alpha-trichosanthin.

KW Chinese cucumber; alpha-trichosanthin; plant virus;  
KW RNA plant virus promoter; systemic infection; foreign gene expression;  
KW AIDS therapeutic drug.

OS Momordica cochinchinensis.

XX US5866785-A.

PN 02-FEB-1999.

PD 07-JUN-1995; 95US-00482920.

XX 26-FEB-1988; 88US-00160766.

PR 26-FEB-1988; 88US-00160771.

PR 15-JUL-1988; 88US-00219279.

PR 17-FEB-1989; 89US-00310881.

PR 05-MAY-1989; 89US-00347637.

PR 08-JUN-1989; 89US-00363138.

PR 22-OCT-1990; 90US-00600244.

PR 16-JAN-1991; 91US-00641617.

PR 26-JUL-1991; 91US-00737899.

PR 01-AUG-1991; 91US-00739143.

PR 31-JUL-1992; 92US-00923692.

PR 19-JAN-1994; 94US-00184237.

XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.

XX Garger SJ, Turpen AM, Grill LK, Grantham GL, Donson J, Dawson WO;

PI Turpen TH;

XX WPI; 1999-142035/12.

DR N-PSDB; AAX03385.

XX Recombinant plant viral vector - that is capable of systemic infection in

PT host plant and stable production of heterologous DNA useful for producing

PT therapeutic proteins for treating e.g. AIDS.

XX Example 4; Col 45-48; 45pp; English.

CC The present sequence represents chinese cucumber alpha-trichosanthin. The  
CC nucleic acid sequence can be expressed in the plant viral constructs of  
CC the invention. The specification describes a recombinant plant viral  
CC nucleic acid derived from a positive (+)-sense RNA plant virus comprising  
CC a native (+)-sense RNA plant virus promoter that is linked to an  
CC expression sequence and a heterologous (+)-sense RNA plant virus promoter  
CC that is linked to an expression sequence. The promoters are incapable of  
CC recombination with each other, and one of the expression sequences  
CC encodes a plant viral coat protein while the other is optionally a  
CC heterologous coding sequence. The plant viral nucleic acid is capable of  
CC systemic infection in a host plant. The viral construct is useful for the  
CC introduction and expression of non-viral foreign genes in plants and the  
CC production of e.g. potential AIDS therapeutic drugs. (Updated on 27-AUG-  
CC 2003 to correct OS field.)

XX Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 2; Length 289;  
Best Local Similarity 99.0%; Pred. No. 1.2e-126;  
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVSLILILFLTPAVEGVDFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60  
DB 1 MIRFLVSLILILFLTPAVEGVDFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60  
QY 61 RSSLPQSORVALIHLTNVADETISVALDVNTVYIMGYRADTSYFNEASATEAAKYVFK 120  
DB 61 RSSLPQSORVALIHLTNVADETISVALDVNTVYIMGYRADTSYFNEASATEAAKYVFK 120  
QY 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSATITLFFYNNASAAALMVLIO 180  
DB 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSATITLFFYNNASAAALMVLIO 180  
QY 181 TSEARARYKTEQOIGKRVDTFLPSLAITSLNSWSLSKOIOIATSTNNGQFETPVVLIN 240  
DB 181 TSEARARYKTEQOIGKRVDTFLPSLAITSLNSWSLSKOIOIATSTNNGQFETPVVLIN 240  
QY 241 AQORVITINVDAGVVTSNIALILNRNNMAAMDVDVPMTOSFGCGSYAI 289  
DB 241 AQORVITINVDAGVVTSNIALILNRNNMAAMDVDVPMTOSFGCGSYAI 289

## RESULT 11

AAW87791  
ID AAW87791 standard; protein; 289 AA.

AC AAW87791;

DT 06-AUG-2003 (revised)

DT 24-AUG-2000 (first entry)

XX Chinese cucumber alpha-trichosanthin protein.

KW Animal RNA virus; viral coat protein; plant; male sterility; interleukin;  
KW EBO; erythropoietin; CSF; colony stimulating factor; Factor VIII; hgm;  
KW human growth hormone; melanin; insulin; vaccine;  
KW stereo specific catalysts; alpha-trichosanthin.

XX Trichosanthes kirilowii.

XX US6054566-A.

PN 25-APR-2000.

PF 07-JUN-1995; 95US-00484341.

PR 26-FEB-1988; 88US-00160766.

PR 26-FEB-1988; 88US-00160771.

PR 15-JUL-1988; 88US-00219279.  
 PR 17-FEB-1989; 89US-00310881.  
 PR 05-MAY-1989; 89US-00347637.  
 PR 08-JUN-1989; 89US-00363138.  
 PR 22-OCT-1990; 90US-00600244.  
 PR 16-JAN-1991; 91US-00641617.  
 PR 26-JUL-1991; 91US-00737899.  
 PR 01-AUG-1991; 91US-00739143.  
 PR 31-JUL-1992; 92US-00923692.  
 XX  
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.  
 XX  
 PI Garger SJ, Grill LK, Turpen TH, Grantham GL, Dawson WO;  
 PI Turpen AM, Donson J;  
 XX  
 DR WPI; 2000-338510/29.  
 DR N-PSDB; AAA12393.  
 XX  
 PT Recombinant non-retroviral nucleic acid for producing proteins such as  
 PT interleukins, melanin and vaccines, comprises subgenomic promoters linked  
 PT to sequences coding for viral coat protein and heterologous proteins.  
 XX  
 PS Example 4; Col 61-62; 51pp; English.  
 XX  
 CC This invention describes a novel recombinant viral nucleic acid (I) from  
 CC a non-retroviral (+) sense, single stranded animal RNA virus comprising a  
 CC nucleic acid sequence coding for a viral coat protein regulated by a  
 CC native subgenomic promoter and other two heterologous nucleic acid  
 CC sequences regulated by two other subgenomic promoters. (I) is useful for  
 CC expressing foreign genes e.g. genes inducing male sterility in plants.  
 CC (I) is also useful for producing proteins such as interleukins, EPO  
 CC (erythropoietin), CSF (colony stimulating factor), Factor VIII, hGH  
 CC (human growth hormone), melanin, insulin, vaccines etc., and enzymes that  
 CC are useful for stereo specific catalysts of organic compounds. (I) is  
 CC stable and transcribed systemically. The dual subgenomic promoter system  
 CC reduces the frequency of recombination thus reducing regeneration of the  
 CC wild type virus. This sequence represents a Chinese cucumber alpha-  
 CC trichosanthin protein which is described in the method of the invention.  
 CC (Updated on 06-AUG-2003 to correct OS field.)  
 CC  
 SQ Sequence 289 AA;  
 XX  
 Query Match 99.2%; Score 1420; DB 3; Length 289;  
 Best Local Similarity 99.0%; Pred. No. 1.2e-126;  
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MRFLVLSLILTLFLTPAVGSDVSPRLSGATSSSYGVFISLRLALPNERKLYDIPLL 60  
 DB 1 MRFLVLSLILTLFLTPAVGSDVSPRLSGATSSSYGVFISLRLALPNERKLYDIPLL 60  
 QY 61 RSSLPSSQRYVALIHLTNVADETISVAIDVTNVYIMGVRAGDTSYFNEASATEAAKYFK 120  
 DB 61 RSSLPSSQRYVALIHLTNVADETISVAIDVTNVYIMGVRAGDTSYFNEASATEAAKYFK 120  
 QY 121 DAMRKVTLPYSGNYERLQTPAGKIRINIPILGLPALDSAITTLFFYVANSAAASALMWLIQS 180  
 DB 121 DAMRKVTLPYSGNYERLQTPAGKIRINIPILGLPALDSAITTLFFYVANSAAASALMWLIQS 180  
 QY 181 TSEAAKYKIEOQIGRVKTPILPSLAITISLENSNALSQKQIOIATNNQGFSPVVLN 240  
 DB 181 TSEAAKYKIEOQIGRVKTPILPSLAITISLENSNALSQKQIOIATNNQGFSPVVLN 240  
 QY 241 AONQRTTNVDAGVVTNSNIALLNENNAAMDDVPMTQSFQCGSYAL 289  
 DB 241 AONQRTTNVDAGVVTNSNIALLNENNAAMDDVPMTQSFQCGSYAI 289  
 XX  
 RESULT 12  
 ADH44106  
 ID ADH44106 standard; protein; 289 AA.  
 XX  
 AC ADH44106;  
 XX

DT 25-MAR-2004 (first entry)  
 XX  
 DE Chinese cucumber alpha-trichosanthin.  
 XX  
 KW RNA; cis-acting replication; RNA plant virus; capped RNA molecule;  
 KW coat gene; movement protein gene; subgenomic promoter;  
 KW herbicide resistance; extreme temperature resistance; drought;  
 KW osmotic stress; pests resistance; male sterility; female sterility;  
 KW yield; collagenase cleavage site; Chinese cucumber; alpha-trichosanthin;  
 KW enzyme; plant.  
 XX  
 OS Trichosanthes kirilowii.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..23  
 FT Peptide /note="Signal peptide"  
 FT Protein 24..289 /note="Mature alpha trichosanthin"  
 FT  
 XX  
 PN US2003150019-A1.  
 PN  
 PD 07-AUG-2003.  
 PD  
 XX  
 PF 24-OCT-2002; 2002US-00280679.  
 PF  
 XX  
 PR 26-FEB-1988; 88US-00160766.  
 PR 26-FEB-1988; 88US-00160771.  
 PR 15-JUL-1988; 88US-00219279.  
 PR 22-OCT-1990; 90US-00600244.  
 PR 16-JAN-1991; 91US-00641617.  
 PR 26-JUL-1991; 91US-00737899.  
 PR 01-AUG-1991; 91US-00739143.  
 PR 31-JUL-1992; 92US-00923692.  
 PR 07-JUN-1995; 95US-00484341.  
 PR 24-APR-2000; 2000US-00557941.  
 XX  
 PA (LARG-) LARGE SCALE BIOLOGY CORP.  
 PA  
 PI Turpen TH, Turpen AM, Garger SJ, Grill LK, Donson J, Dawson WO;  
 PI Grantham GL;  
 XX  
 DR WPI; 2003-897624/82.  
 DR N-PSDB; ADH44105.  
 XX  
 PT New recombinant viral RNA molecules, useful in modifying a plant host  
 PT cell, genotypically or phenotypically, e.g. male sterility or improved  
 PT resistance to pests or diseases, or for producing pharmaceuticals,  
 PT hormones or antidotes.  
 XX  
 PS Example 4; SEQ ID NO 4; 50pp; English.  
 XX  
 CC The invention relates to an RNA molecule (RVNA) comprising a cis-acting  
 CC replication element from a positive strand RNA plant virus capable of  
 CC replication in a plant cell and comprising an exogenous RNA segment  
 CC capable of expressing its function in a host cell. The exogenous RNA  
 CC segment is located in a region of the RNA molecule able to tolerate the  
 CC segment without disrupting RNA replication in the absence of a trans-  
 CC acting replication element in the host cell. Also included are a capped  
 CC RNA molecule capable of infecting a host plant cell (where the capped RNA  
 CC molecule: (a) comprises a cis-acting replication element derived from a  
 CC positive strand RNA plant virus, has no extraneous non-viral sequences  
 CC between the cap site and the 5' terminus of the viral sequence, and  
 CC further comprises an exogenous RNA segment capable of expressing its  
 CC function in a host cell in a region of the capped RNA molecule able to  
 CC tolerate the segment without disrupting RNA replication of the capped RNA  
 CC molecule in the absence of a trans-acting replication element in the host  
 CC cell; or (b) has no extraneous non-viral sequences between the cap site  
 CC and the 5' terminus of the viral sequence, and where the capped RNA  
 CC molecule comprises the entire genome of the positive strand RNA virus,  
 CC such as Iteovirus, potexvirus, potyvirus, tombusvirus, tymovirus and  
 CC tobamovirus, carmovirus, or sobemovirus, and an exogenous RNA segment  
 CC capable of expressing its function in a host cell, where the exogenous  
 CC RNA segment inserted into the genome of the positive strand RNA virus at

CC a gene site consisting of a coat gene site, a movement protein gene site,  
 CC or another gene site under the control of a subgenomic promoter, which is  
 CC one of at least two subgenomic promoters present in the virus), a DNA  
 CC transcription vector comprising cDNA having one strand complementary to  
 CC the (capped) RNA molecule cited above and methods of modifying a host  
 CC cell, genotypically or phenotypically (comprising introducing into the  
 CC cell the (capped) RNA molecule cited above, where the exogenous RNA  
 CC segment confers a detectable trait in the host cell which modifies the  
 CC host cell). The cis-acting replication element is derived from a  
 CC monopartite plant virus, tobamovirus, or tobacco mosaic virus. The  
 CC (capped) RNA molecules and DNA transcription vectors are useful in  
 CC modifying a host cell, genotypically or phenotypically, e.g. improved  
 CC tolerance to herbicides, extremes of heat or cold, drought or osmotic  
 CC stress, improved resistance to pests or diseases, male or female  
 CC sterility, or improved yield. The RNA molecules are also useful for  
 CC transcription or expression of foreign genes in the host to produce the  
 CC desired product, such as pharmaceuticals, hormones, antibiotics,  
 CC pigments, or antibodies. The present sequence is encoded by the Chinese  
 CC cucumber alpha-trichosanthin cDNA, which was used as the exogenous RNA in  
 CC an RNAV of the invention.

CC Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 7; Length 289;  
 Best Local Similarity 99.0%; Pred. No. 1,2e-126;  
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVLSLILTLFLTPAVGDSFRLSGATSSSYGVFISNLRKALPNERKLYDIPPL 60  
 DB 1 MIRFLVLSLILTLFLTPAVGDSFRLSGATSSSYGVFISNLRKALPNERKLYDIPPL 60  
 QY 61 RSSLPSSQRYALHLTNVADETSVAIDVTNVIMYGRAGDTSYFNEASATEAKYVFK 120  
 DB 61 RSSLPSSQRYALHLTNVADETSVAIDVTNVIMYGRAGDTSYFNEASATEAKYVFK 120  
 QY 121 DAMRKVTLPSYSGNVERLQTAAGKIRENIPGLPALDSATITLFFYNANSAASALMWLIQS 180  
 DB 121 DAMRKVTLPSYSGNVERLQTAAGKIRENIPGLPALDSATITLFFYNANSAASALMWLIQS 180  
 QY 181 TSEARARYKFEIQIGKRVKTFPLPSLAIIISLENSWSALSKQIQIASTNNQGFETPVVLIN 240  
 DB 181 TSEARARYKFEIQIGKRVKTFPLPSLAIIISLENSWSALSKQIQIASTNNQGFETPVVLIN 240  
 QY 241 AONORVITTVNDAGVTSNIALILNRNMAAMDVDVMTQSFQCGSYAI 289  
 DB 241 AONORVITTVNDAGVTSNIALILNRNMAAMDVDVMTQSFQCGSYAI 289

# RESULT 13

ADO43821  
 ID ADO43821 standard; protein; 289 AA.

AC ADO43821;

DT 15-JUL-2004 (first entry)

DE Chinese cucumber alpha-trichosanthin.

XX recombinant viral nucleic acid; animal virus; subgenomic promoter;  
 KM viral coat protein; IL-1; IL-2; IL-3; IL-4; IL-5; IL-6; IL-7; IL-8; IL-9;  
 KM IL-10; IL-11; IL-12; EPO; G-CSF; GM-CSF; M-CSF; Factor VIII; Factor IX;  
 KM tissue plasminogen activator; human growth hormone; neuro-peptide;  
 KM melatonin; lipase; hormone; pharmaceutical; antibiotic; vaccine; insulin;  
 KM Chinese cucumber; alpha-trichosanthin.

XX Trichosanthes kirilowii.

XX US2004049025-A1.

XX 11-MAR-2004.

XX 24-OCT-2002; 2002US-00280725.

XX

PR 26-FEB-1988; 88US-00160766.  
 PR 26-FEB-1988; 88US-00160771.  
 PR 15-JUL-1988; 88US-00219279.  
 PR 17-FEB-1989; 89US-00310881.  
 PR 05-MAY-1989; 89US-00347637.  
 PR 08-JUN-1989; 89US-00363138.  
 PR 22-OCT-1990; 90US-00600244.  
 PR 16-JAN-1991; 91US-00641617.  
 PR 26-JUL-1991; 91US-00737899.  
 PR 01-AUG-1991; 91US-00739143.  
 PR 31-JUL-1992; 92US-00923692.  
 PR 07-JUN-1995; 95US-00484341.  
 PR 24-Apr-2000; 2000US-00557941.

(LARG-) LARGE SCALE BIOLOGY CORP.

PI Donson J, Dawson WO, Grantham GL, Turpen TH, Turpen AM;

PI Garger SJ, Grilli LK;

DR WPI; 2004-238515/22.

DR N-PSDB; ADO43820.

PT New recombinant viral nucleic acid derived from an animal virus having a  
 PT native subgenomic promoter, useful in production of products such as  
 PT interleukins, enzymes, and hormones.

PS Example 4; SEQ ID NO 4; 49pp; English.

XX The invention describes a recombinant viral nucleic acid derived from an  
 CC animal virus possessing a native subgenomic promoter. The recombinant  
 CC viral nucleic acid comprises: a first viral sub genomic promoter; a first  
 CC nucleic acid sequence that codes for a viral coat protein whose  
 CC transcription is regulated by the first viral subgenomic promoter; a  
 CC second viral sub genomic promoter; and a second nucleic acid sequence  
 CC whose transcription is regulated by the second viral sub genomic  
 CC promoter. Where the first and second viral subgenomic promoters possess  
 CC different nucleic acid sequences relative to each other, and the second  
 CC nucleic acid sequence is upstream to the first nucleic acid sequence.  
 CC Also described are: a non-human host animal infected by a viral vector  
 CC comprising the recombinant viral nucleic acid; and a process for  
 CC transcribing a nucleic acid sequence in a non-human host animal. The  
 CC recombinant viral nucleic acid is useful in a sustained systemic  
 CC transcription of nucleotide sequences within host cells and in producing  
 CC gene products, e.g. IL-1-12, EPO, G-CSF, GM-CSF, M-CSF, Factor VIII,  
 CC Factor IX, tissue plasminogen activator, human growth hormone, receptors,  
 CC receptor antagonists, antibodies, neuro-peptides, melatonin, lipase,  
 CC hormones, pharmaceuticals, antibiotics, vaccines and insulin within a  
 CC host animal. This is the amino acid sequence of Chinese cucumber alpha-  
 CC trichosanthin that can be incorporated into the recombinant viral protein  
 CC of the invention.

XX Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 8; Length 289;  
 Best Local Similarity 99.0%; Pred. No. 1,2e-126;  
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVLSLILTLFLTPAVGDSFRLSGATSSSYGVFISNLRKALPNERKLYDIPPL 60  
 DB 1 MIRFLVLSLILTLFLTPAVGDSFRLSGATSSSYGVFISNLRKALPNERKLYDIPPL 60  
 QY 61 RSSLPSSQRYALHLTNVADETSVAIDVTNVIMYGRAGDTSYFNEASATEAKYVFK 120  
 DB 61 RSSLPSSQRYALHLTNVADETSVAIDVTNVIMYGRAGDTSYFNEASATEAKYVFK 120  
 QY 121 DAMRKVTLPSYSGNVERLQTAAGKIRENIPGLPALDSATITLFFYNANSAASALMWLIQS 180  
 DB 121 DAMRKVTLPSYSGNVERLQTAAGKIRENIPGLPALDSATITLFFYNANSAASALMWLIQS 180  
 QY 181 TSEARARYKFEIQIGKRVKTFPLPSLAIIISLENSWSALSKQIQIASTNNQGFETPVVLIN 240  
 DB 181 TSEARARYKFEIQIGKRVKTFPLPSLAIIISLENSWSALSKQIQIASTNNQGFETPVVLIN 240

QY 241 AONORVTITNVDAVGTSTNIALLLNRRNNMAADDVPMTOGFCGSGYAL 289  
 DB 241 AONORVMTITNVDAVGTSTNIALLLNRRNNMAADDVPMTOGFCGSGYAL 289

## RESULT 14

AA032986  
 ID AAR32986 standard; protein; 289 AA.  
 XX  
 AC AAR32986;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 17-JUN-1993 (first entry)  
 XX

DE Encodes chinese cucumber alpha-trycosanthin.

KW Recombinant products; commercial production; fermentation; biosynthesis;  
 KW natural products; recombinant proteins; product expression;  
 KW protein expression; expressed proteins.

OS Cucurbitaceae.

XX MO9303161-A1.

XX 18-FEB-1993.

XX 31-JUL-1992; 92WO-US06359.

XX 01-AUG-1991; 91US-00739143.

XX (DONS/) DONSON J.

XX (DAMS/) DAMSON W O.

XX (GRAN/) GRANTHAM G L.

XX (TURP/) TURPEN T H.

XX (GARG/) GARGER S J.

XX (GRIL/) GRILLE L K.

XX Donson J, Dawson MO, Grantham GL, Turpen TH, Turpen AM;

XX Garger SJ, Grille LK;

XX WPI; 1993-076518/09.

XX N-PSDB; AAQ37679.

XX Recombinant plant viral nucleic acids - used to express a prod., e.g.

XX antibody or IL-1 in a plant.

XX Example 4; Page 96; 30pp; English.

XX This sequence represents chinese cucumber alpha-trycosanthin. The coding

XX sequence is inserted into a recombinant plant viral nucleic acid which is

XX then used to express a recombinant product (in this case alpha-

XX trycosanthin) in a plant. The plant viral sequence may be from tobacco

XX mosaic, cucumber green mottle, cowpea mosaic, brome mosaic, broad bean

XX mottle, rice necrosis, geminiviruses, tomato golden mosaic, Cassava

XX latent and maize streak viruses. (Updated on 25-MAR-2003 to correct PN

XX field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-

XX 2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 289 AA;

XX Query Match 99.0%; Score 1417; DB 2; Length 289;

XX Best Local Similarity 98.6%; Pred. No. 2.3e-126;

XX Matches 285; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVLSLLILTLFTTPAVEGDSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60

DB 1 MIRFLVLSLLILTLFTTPAVEGDSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60

QY 61 RSLPSGQRXALHILNTNVADETISVAIDVTNVYIMGYRAGDTSYFENASATEAKYVFK 120

DB 61 RSLPSGQRXALHILNTNVADETISVAIDVTNVYIMGYRAGDTSYFENASATEAKYVFK 120

QY 121 DAMRKVTLPYSGNRYERLQTAAGKIRENIPLGHPALDSAITTLFPYNNANSAALNVLIOG 180  
 DB 121 DAMRKVTLPYSGNRYERLQTAAGKIRENIPLGHPALDSAITTLFPYNNANSAALNVLIOG 180

QY 181 TSEARXYKFEIOQIGKRVDTFLPSLAIISLENSWSALSKQIQIASTNNQGFESPVLIN 240

DB 181 TSEARXYKFEIOQIGKRVDTFLPSLAIISLENSWSALSKQIQIASTNNQGFESPVLIN 240

QY 241 AONORVTITNVDAVGTSTNIALLLNRRNNMAADDVPMTOGFCGSGYAL 289

DB 241 AONORVMTITNVDAVGTSTNIALLLNRRNNMAADDVPMTOGFCGSGYAL 289

## RESULT 15

AA07523  
 ID AAR07523 standard; protein; 289 AA.

XX AAR07523;  
 XX

XX 06-FEB-1991 (first entry)

XX Alpha-Trichosanthin encoded by insert sequence from clone 12.

XX Trichosanthin (TCS); Human Immunodeficiency Virus; inhibition.

XX Trichosanthes kirilowii.

XX Key Location/Qualifiers

XX FT Region 1..23

XX FT Protein /label= signal peptide

XX FT Protein /label= alpha-TCS

XX WO9012097-A.

XX 18-OCT-1990.

XX 04-APR-1989; 89US-00333184.

XX 04-APR-1989; 89US-00333184.

XX (GENB-) GENELABS INC.

XX Platek M, Chow T, Fry K;

XX WPI; 1990-334847/44.

XX N-PSDB; AAQ06351.

XX Recombinant tri:chosanthin protein - with selective inhibitory effect on

XX viral expression in HIV infected T-cells or monocyte-macrophase.

XX Example; Fig 20; 102pp; English.

XX PQ30B was used as a probe to identify clones containing sequences coding

XX for TCS in a T.kirilowii genomic library. Five clones were eventually

XX isolated and sequenced, including clone 12. They were found to have

XX homology to the alpha-TCS coding sequence. See also AAQ06343-Q06350

XX Sequence 289 AA;

XX Query Match 93.2%; Score 1333; DB 2; Length 289;

XX Best Local Similarity 92.7%; Pred. No. 2.3e-118;

XX Matches 268; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 MIRFLVLSLLILTLFTTPAVEGDSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60

DB 1 MIRFLVLSLLILTLFTTPAVEGDSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60

QY 61 RSLPSGQRXALHILNTNVADETISVAIDVTNVYIMGYRAGDTSYFENASATEAKYVFK 120

DB 61 RSLPSGQRXALHILNTNVADETISVAIDVTNVYIMGYRAGDTSYFENASATEAKYVFK 120



QY 121 DAMKVTLPYSGNVERLOTAAGKIRENIPGLPALDSAITTLFYNNANSASALMWLIQS 180  
DB 121 DAQRKVTLPYSGNVERLOTAAGKIRENIPGLPALDSAITNLFYNNANSASALMWLIQS 180  
QY 181 TSEARARYKFEQOIGKRVDTFLPSLAISLENSWSALSQOIASTNNGQFESPVLIN 240  
DB 181 MSEARARYKFEQOIGRVRDTFLPSLAISLENSWSALSQOIASTNNGQFETPVVLIN 240  
QY 241 AQORVTITNVDAGVVTSNIALLLNRNNMAMDDVPMQTSGCGSYAL 289  
DB 241 AQORVTITNVDAGVVTSNIALLLNRNNMAVIDDHVPMQSGCGSYAI 289

Search completed: April 12, 2005, 15:09:59  
Job time : 133.481 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 12, 2005, 14:56:17 ; Search time 125.09 seconds

(without alignments)  
1183.080 Million cell updates/sec

Title: US-09-905-247A-1

Perfect score: 1431

Sequence: 1 MRFLVLSLILFLTPA.....AAMDVVPMQSRGCSYAL 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1429	99.9	289	1	RIP1 TRIKI
2	1426	99.7	289	2	Q845T8
3	1425	99.6	289	2	Q94KE4
4	1415	98.9	289	2	Q41216
5	1384	96.7	289	1	RIPS TRIKI
6	1269	88.7	270	2	Q41611
7	1264	88.3	270	2	Q6PRG5
8	1260	88.1	270	2	Q8LPV7
9	1195	83.5	247	2	Q6BBQ4
10	1187	82.9	247	2	Q9LRE3
11	1171.5	81.9	290	1	RIP1 BRDYI
12	866.5	60.6	286	1	RIP1_MOMCH
13	809.5	56.6	277	1	RIP1_LUCY
14	782	54.6	278	2	Q00980
15	764	53.4	286	1	RIP3_MOMCH
16	762	53.2	286	1	RIP2_MOMBA
17	743	51.9	286	1	RIP1_CUCFI
18	711	49.7	254	1	Q684T5
19	682.5	47.7	294	1	RIP1_TRIAN
20	680	47.5	250	1	RIP1_LUCY
21	540.5	37.8	282	1	RIP2_BRDYI
22	476.5	33.3	136	2	Q8SAD7
23	439.5	30.7	563	2	Q8G7J2
24	435.5	30.4	563	2	Q945S2
25	434.5	30.4	563	1	NIGB_SAMNT
26	432.5	30.2	563	2	Q04367
27	425	29.7	541	2	Q41174
28	421	29.4	576	1	RICI RICCO
29	418.5	29.2	275	1	Q8H1Y4
30	416.5	29.1	564	2	Q9AVR2
31	415.5	29.0	136	2	Q8SAG0

32	414	28.9	580	2	Q94BW4	Q94BW4 cinanomum
33	410	28.7	580	2	Q94BW3	Q94BW3 cinanomum
34	407.5	28.5	275	2	Q84LJ1	Q84LJ1 gnostemma
35	407	28.4	581	2	Q94BW5	Q94BW5 cinanomum
36	403.5	28.2	277	2	Q8GV09	Q8GV09 gnostemma
37	403.5	28.2	549	2	Q9FV22	Q9FV22 cinanomum
38	401.5	28.1	277	2	Q84JRI	Q84JRI gnostemma
39	400.5	28.0	277	2	Q8GV11	Q8GV11 gnostemma
40	396.5	27.7	564	1	AGEL_RICCO	P06750 ricinus com
41	395.5	27.6	277	2	Q8H1Y5	Q8H1Y5 gnostemma
42	393.5	27.5	136	2	Q84LJ0	Q84LJ0 cucurbita m
43	392.5	27.4	136	2	Q84LI9	Q84LI9 cucurbita m
44	388.5	27.1	277	2	Q8GV10	Q8GV10 gnostemma
45	384.5	26.9	136	2	Q8S2R5	Q8S2R5 cucurbita m

## ALIGNMENTS

RESULT 1  
RIP1 TRIKI STANDARD; PRT; 289 AA.  
AC P09989;  
AD RIP1 TRIKI  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ribosome-inactivating protein alpha-trichosanthin precursor  
DE (EC 3.2.2.22) (tRNA N-glycosidase) (Alpha-TCS).  
OS Trichosanthes kirilowii (Mongolian snake-gourd).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroside I; Cucurbitales; Cucurbitaceae; Trichosanthes.  
OX NCBI\_TaxID=3677;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Maximowicz;  
RX MEDLINE=91153657; PubMed=1999291; DOI=10.1016/0378-1119(91)90061-F;  
RA Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;  
RT "Cloning of trichosanthin cDNA and its expression in Escherichia coli.";  
RT coll.";  
RN [2]  
RN Gene 97:267-272(1991).  
RN [3]  
RN SEQUENCE FROM N.A.  
RC STRAIN=Maximowicz; TISSUE=Leaf;  
RX MEDLINE=90256790; PubMed=2341400;  
RA Chow T., Feldman R.A., Lovett M., Piatek M.;  
RT "Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I ribosome-inactivating protein.";  
RT J. Biol. Chem. 265:8670-8674(1990).  
RN [4]  
RN SEQUENCE OF 24-270.  
RC STRAIN=Maximowicz; TISSUE=Tuberous root;  
RX MEDLINE=90256789; PubMed=2341399;  
RA Collins E.J., Roberts J.D., Lopresti M., Stone K.L., Williams K.R.,  
RT "Primary amino acid sequence of alpha-trichosanthin and molecular models for abrin A-chain and alpha-trichosanthin.";  
RT J. Biol. Chem. 265:8665-8669(1990).  
RN [5]  
RN SEQUENCE OF 24-270.  
RC TISSUE=tuberous root;  
RA Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,  
RT Tian G.Y., Ni C.Z.;  
RT "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application.";  
RT Pure Appl. Chem. 58:789-798(1996).  
RN [6]  
RN X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).  
RX MEDLINE=9434957; PubMed=8066085;  
RA Zhou F., Fu Z., Chen M., Lin Y., Pan K.;  
RT "Structure of trichosanthin at 1.88-A resolution.";  
RT Proteins 19:4-13(1994).

RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RA MEDLINE=95344383; PubMed=7619070;  
 RX Huang Q., Liu S., Tang Y., Jin S., Wang Y.;  
 RT "Studies on crystal structures, active-centre geometry and  
 RT dephurinating mechanism of two ribosome-inactivating proteins.";  
 RL Biochem.J. 309:285-298(1995).  
 CC -1- FUNCTION: Trichosanthin is an abortion-inducing protein. It is  
 CC capable of inhibiting HIV-1 infection and replication. It  
 CC inactivates eukaryotic 60S ribosomal subunits.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
 CC Type 1 RIP subfamily.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M34858; AAA34207.1; -;  
 DR EMBL: J05434; AAA34206.1; -;  
 DR PIR: J0566; RUPRT.  
 DR PDB: 1GIS; X-ray; A=23-270.  
 DR PDB: 1GIU; X-ray; A=24-270.  
 DR PDB: 1JAG; X-ray; A/B/C/D=23-270.  
 DR PDB: 1MRJ; X-ray; @=24-270.  
 DR PDB: 1MRK; X-ray; @=24-270.  
 DR PDB: 1NLI; X-ray; A=23-270.  
 DR PDB: 1OD2; X-ray; A=24-270.  
 DR PDB: 1TCS; X-ray; @=24-270.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP. 1  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW 3d-structure; Antiviral; Direct protein sequencing; Hydrolase;  
 KW Plant defense; Protein synthesis inhibitor; Signal; Toxin.  
 FT FT CHAIN 1 23  
 FT FT SIGNAL 24 270  
 FT FT PROPEP 271 289  
 FT FT ACT SITE 183 183  
 FT FT CONFLICT 57 60  
 FT FT CONFLICT 82 84  
 FT FT CONFLICT 87 87  
 FT FT CONFLICT 92 92  
 FT FT CONFLICT 143 144  
 FT FT CONFLICT 196 196  
 FT FT CONFLICT 215 216  
 FT FT CONFLICT 231 231  
 FT FT CONFLICT 234 234  
 FT FT CONFLICT 246 246  
 FT FT CONFLICT 247 247  
 FT FT STRAND 25 28  
 FT FT TURIN 30 31  
 FT FT HELIX 34 46  
 FT FT TURIN 47 47  
 FT FT TURIN 50 54  
 FT FT TURIN 55 56  
 FT FT STRAND 57 60  
 FT FT HELIX 66 69  
 FT FT STRAND 70 76  
 FT FT TURIN 78 79  
 FT FT STRAND 82 88  
 FT FT TURIN 89 92  
 FT FT STRAND 93 99  
 FT FT TURIN 100 101  
 FT FT STRAND 102 105  
 FT FT HELIX 109 114  
 FT FT TURIN 115 117  
 FT FT TURIN 120 121

Removed in mature form.  
 By similarity.  
 IPLL -> LPLI (in Ref. 4).  
 Missing (in Ref. 4).  
 I -> L (in Ref. 4).  
 V -> VDAGPRNAVL (in Ref. 4).  
 KI -> GL (in Ref. 4).  
 K -> S (in Ref. 4).  
 WS -> LML (in Ref. 4).  
 Q -> T (in Ref. 2).  
 S -> T (in Ref. 2).  
 Missing (in Ref. 4).  
 T -> M (in Ref. 2).

Ribosome-inactivating protein alpha-trichosanthin.

FT STRAND 124 127  
 FT HELIX 134 141  
 FT TURIN 142 142  
 FT HELIX 145 147  
 FT STRAND 150 150  
 FT HELIX 152 163  
 FT TURIN 164 165  
 FT HELIX 167 180  
 FT TURIN 181 181  
 FT HELIX 182 186  
 FT STRAND 187 197  
 FT HELIX 188 195  
 FT TURIN 196 196  
 FT STRAND 202 202  
 FT HELIX 206 226  
 FT TURIN 227 230  
 FT STRAND 231 239  
 FT TURIN 241 242  
 FT STRAND 245 250  
 FT TURIN 251 252  
 FT HELIX 254 258  
 FT TURIN 259 259  
 FT STRAND 260 260  
 FT STRAND 263 263  
 FT TURIN 266 268

SEQUENCE 289 AA; 31676 MW; 5CE09BB630575BB9 CRC64;  
 SQ  
 Query Match 99.9%; Score 1429; DB 1; Length 289;  
 Best Local Similarity 99.7%; Pred. No. 8,3e-104;  
 Matches 288; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIRFLVSLILITLTLTPPAVEGDVSFRLSGATSSGVFISLNLRKALPNERKLYDIFLL 60  
 DB 1 MIRFLVSLILITLTLTPPAVEGDVSFRLSGATSSGVFISLNLRKALPNERKLYDIFLL 60

QY 61 RSSLPQSQRVYALIHNTYADETISVAIDVTNYIINGYRPAAGTSTYFENASATEAKYVK 120  
 DB 61 RSSLPQSQRVYALIHNTYADETISVAIDVTNYIINGYRPAAGTSTYFENASATEAKYVK 120

QY 121 DMRKVYTLPSGNYVERLQTPAGKIRENTPLGIPALDSATITLFFYNNASASALMWLIQS 180  
 DB 121 DMRKVYTLPSGNYVERLQTPAGKIRENTPLGIPALDSATITLFFYNNASASALMWLIQS 180

QY 181 TSEARVYFIEQIKRYDKTFPLPSLAISLNSWSALSKOIQIASTNNGOFESPVLIN 240  
 DB 181 TSEARVYFIEQIKRYDKTFPLPSLAISLNSWSALSKOIQIASTNNGOFESPVLIN 240

QY 241 AONQRTVTITNDAGVVTSTNIALLLNRNNMAAMDVVPMTOFGCGSYAL 289  
 DB 241 AONQRTVTITNDAGVVTSTNIALLLNRNNMAAMDVVPMTOFGCGSYAL 289

RESULT 2  
 Q84SV8 PRELIMINARY; PRT; 289 AA.  
 AC Q84SV8;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Trichosanthin.  
 GN Name=TCS;  
 OS Trichosanthes kirilowii (Mongolian snake-gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC euroside 1; Cucurbitales; Cucurbitaceae; Trichosanthes.  
 OC NCBI\_TaxID=3677;  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RA Yuan H., Wang L., Wang Y., Liu T., An C., Chen Z.;  
 RL Submitted (MAR-2003) to the EMBL/Genbank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.

DR EMBL: AY082349; AAC72728.1; -.  
 DR HSP: P09989; 1MRJ.  
 DR GO: GO:0016787; F:hydrolase activity; IEA.  
 DR GO: GO:0030598; F:RNA N-glycosylase activity; IEA.  
 DR GO: GO:0006952; P:defense response; IEA.  
 DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
 DR GO: GO:0009405; P:pathogenesis; IEA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
 DR HydroLase: Plant defense; Protein synthesis inhibitor; Toxin.  
 SQ SEQUENCE 289 AA; 31690 MW; B403148E96861PA CRC64; 1

Query Match 99.7%; Score 1426; DB 2; Length 289;  
 Best Local Similarity 99.3%; Pred. No. 1,4e-103;  
 Matches 287; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIRFLVSLILILFLTPPAVEGVSPRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60  
 DB 1 MIRFLVSLILILFLTPPAVEGVSPRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60  
 QY 61 RSSLPQSORYALHLTNVADETISVAIDVTNVIIMGYRAGDTSYFFNEASATEAAKVF 120  
 DB 61 RSTLPQSORYALHLTNVADETISVAIDVTNVIIMGYRAGDTSYFFNEASATEAAKVF 120  
 QY 121 DANRKYTLPSYSGNYERLQTPAGKIRENIPGLPALDSATITLTFYNNASASALMVLIO 180  
 DB 121 DANRKYTLPSYSGNYERLQTPAGKIRENIPGLPALDSATITLTFYNNASASALMVLIO 180  
 QY 181 TSEAAKYKTEEOIGKRVDTFLPSLAITSLNSWSALSKQIOIASTNNGQFSPVVLIN 240  
 DB 181 TSEAAKYKTEEOIGKRVDTFLPSLAITSLNSWSALSKQIOIASTNNGQFSPVVLIN 240  
 QY 241 AQNRVTITNVDAVGVTSNIALILNRNMAAMDVDVPMTOGFCGSGYAI 289  
 DB 241 AQNRVTITNVDAVGVTSNIALILNRNMAAMDVDVPMTOGFCGSGYAI 289

RESULT 3  
 Q94KE4 PRELIMINARY; PRT; 289 AA.  
 AC 094KE4;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Trichosanthin precursor.  
 GN Name=TCS;  
 OS Trichosanthes kirilowii (Mongolian snake-gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid 1; Cucurbitales; Cucurbitaceae; Trichosanthes.  
 NC NCBI\_TaxID=3677;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yuan H., Wang Y., An C., Chen Z.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 specific adenosine on the 28S rRNA.  
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
 DR EMBL: AF367252; AA052860.1; -.  
 DR PIR: JC5032; JC5032.  
 DR HSP: P09989; 1MRJ.  
 DR GO: GO:0016787; F:hydrolase activity; IEA.  
 DR GO: GO:0030598; F:RNA N-glycosylase activity; IEA.  
 DR GO: GO:0006952; P:defense response; IEA.  
 DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
 DR GO: GO:0009405; P:pathogenesis; IEA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
 KM HydroLase: Plant defense; Protein synthesis inhibitor; Signal; Toxin.

FT SIGNAL 1 23 Potential.  
 FT CHAIN 24 270 trichosanthin.  
 SQ SEQUENCE 289 AA; 31706 MW; A6D5602549CA557 CRC64; 1

Query Match 99.6%; Score 1425; DB 2; Length 289;  
 Best Local Similarity 99.0%; Pred. No. 1,7e-103;  
 Matches 286; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIRFLVSLILILFLTPPAVEGVSPRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60  
 DB 1 MIRFLVSLILILFLTPPAVEGVSPRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60  
 QY 61 RSSLPQSORYALHLTNVADETISVAIDVTNVIIMGYRAGDTSYFFNEASATEAAKVF 120  
 DB 61 RSTLPQSORYALHLTNVADETISVAIDVTNVIIMGYRAGDTSYFFNEASATEAAKVF 120  
 QY 121 DANRKYTLPSYSGNYERLQTPAGKIRENIPGLPALDSATITLTFYNNASASALMVLIO 180  
 DB 121 DSNRKYTLPSYSGNYERLQTPAGKIRENIPGLPALDSATITLTFYNNASASALMVLIO 180  
 QY 181 TSEAAKYKTEEOIGKRVDTFLPSLAITSLNSWSALSKQIOIASTNNGQFSPVVLIN 240  
 DB 181 TSEAAKYKTEEOIGKRVDTFLPSLAITSLNSWSALSKQIOIASTNNGQFSPVVLIN 240  
 QY 241 AQNRVTITNVDAVGVTSNIALILNRNMAAMDVDVPMTOGFCGSGYAI 289  
 DB 241 AQNRVTITNVDAVGVTSNIALILNRNMAAMDVDVPMTOGFCGSGYAI 289

RESULT 4  
 Q41216 PRELIMINARY; PRT; 289 AA.  
 ID Q41216;  
 AC Q41216;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Trichosanthin.  
 GN Name=trichosanthin; Synonyms=TCS;  
 OS Trichosanthes kirilowii (Mongolian snake-gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid 1; Cucurbitales; Cucurbitaceae; Trichosanthes.  
 NC NCBI\_TaxID=3677;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=94271613; PubMed=8003348;  
 RX Zheng H., Wang B., Shaw P., Yeung H.;  
 RT "Cloning and DNA sequencing of the gene encoding trichosanthin.";  
 RL I Chuan Hsueh Pao 21:42-51(1994).  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 specific adenosine on the 28S rRNA.  
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
 DR EMBL: S70176; AAB31048.1; -.  
 DR PIR: JC5032; JC5032.  
 DR HSP: P09989; 1J4G.  
 DR GO: GO:0030598; F:RNA N-glycosylase activity; IEA.  
 DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
 KM HydroLase: Plant defense; Protein synthesis inhibitor; Toxin.  
 SQ SEQUENCE 289 AA; 31650 MW; 286AC14D48BCA175 CRC64; 1

Query Match 98.9%; Score 1415; DB 2; Length 289;  
 Best Local Similarity 98.3%; Pred. No. 1e-102;  
 Matches 284; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIRFLVSLILILFLTPPAVEGVSPRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60  
 DB 1 MIRFLVSLILILFLTPPAVEGVSPRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60  
 QY 61 RSSLPQSORYALHLTNVADETISVAIDVTNVIIMGYRAGDTSYFFNEASATEAAKVF 120

Dd		61	RSLPGSGRYALVHLITNVADEITVAIDVTSTYINGTAAGDTSYFFNSAATAAKVIYFK	120
Oy		121	DAMKRVTLPYSGNVERLQTPAGKIRENIPLGLPALDSAITLLFYNNASAALMVLIQS	180
Dd		121	DAMKRVTLPYSGNVERLQTPAGKIRENIPLGIPALDSAITLLFYNNASAALMVLIIQS	180
Oy		181	TSEARARYETFIQQIGKVDKTFPLPSLAITSLENSMSALSQIQAISTNGGFESPVLTIN	240
Dd		181	TSEARARYETFIQQIGKVDKTFPLPSLAITSLENSMSALSQIQAISTNGGFEPVVLIN	240
Oy		241	AQNQRVTITNDAGVVTSNIALLLNRNMMAAMDDEVPTQSPFGCSVAL	289
Dd		241	AQNQRVTITNDAGVVTSNIALLLNRNMMAAMDDEVPTQSFCCGSIAI	289
RESULT 5				
RIPS_TRIKI	ID	RIPS_TRIKI	STANDARD;	PRT; 289 AA.
AC		p24478;		
Dt		01-MAR-1992	(Rel. 21, Created)	
Dt		15-DEC-1998	(Rel. 37, Last sequence update)	
Dt		05-JUL-2004	(Rel. 44, Last annotation update)	
Dt		De	Ribosome-inactivating protein karasurin precursor (BC 3.2.2.22) (rRNA N-glycosylase).	
Os		Trichosanthes kirilowii	(Mongolian snake-gourd).	
Oc		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
Oc		Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
Ox		eurosid I; Cucurbitales; Cucurbitaceae; Trichosanthes.		
NX		NCBI_TaxId=3677;		
Rn		[1]		
Rp		SEQUENCE FROM N.A.		
Rc		TISSUE=Root tuber;		
Rx		MEDLINE=97356562; PubMed=9212998;		
Ra		Mizukami H., Iida K., Kondo T., Ogihara Y.;		
Rt		"Cloning and bacterial expression of a gene encoding ribosome-		
Rt		inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes		
Rl		kirilowii var. japonica.";		
Rl		Biol. Pharm. Bull. 20:711-713(1997).		
Rn		[2]		
Rp		SEQUENCE OF 24-270.		
Rp		MEDLINE=92005921; PubMed=1914000;		
Ra		Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;		
Rt		"The complete amino acid sequence of an abortifacient protein,		
Rt		karasurin.";		
Rl		Chem. Pharm. Bull. 39:1244-1249(1991).		
Cc	-	FUNCTION: Aborton-inducing protein. It inactivates eukaryotic 60S		
Cc	-	ribosomal subunits.		
Cc	-	CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one		
Cc	-	specific adenosine on the 28S rRNA.		
Cc	-	SIMILARITY: Belongs to the ribosome-inactivating protein family.		
Cc	-	Type 1 RIP subfamily.		
Cc	-	-----		
Cc	-	THIS SWISS-PROT entry is copyright. It is produced through a collaboration		
Cc	-	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
Cc	-	the European Bioinformatics Institute. There are no restrictions on its		
Cc	-	use by non-profit institutions as long as its content is in no way		
Cc	-	modified and this statement is not removed. Usage by and for commercial		
Cc	-	entities requires a license agreement (see http://www.isb-sib.ch/announce/		
Cc	-	or send an email to license@isb-sib.ch).		
Cc	-	-----		
Dd		EMBL; AB000666; BAA21786.1; --		
Dd		PIR; JC5606; JC5606.		
Dd		PIR; J00393; J00393.		
Dd		HSSP; P09989; IMRJ.		
Dd		InterPro; IPRO01574; RIP.		
Dd		Pfam; PF00161; RIP.1.		
Dd		PRINTS; PR00396; SHIGARICIN.		
Dd		PROSITE; PS00275; SHIGA_RICIN_1.		
Kw		Antiviral; Direct protein sequencing; Hydrolase; Plant defense;		
Kw		protein synthesis inhibitor; Signal; Toxin.		
Rt		SIGNAL	1 21	
Rt		CHAIN	22 270	Ribosome-inactivating protein karasurin-

FT	CHAIN	24	270	C. Ribosome-inactivating protein karasurin-A.
FT	PROPER	271	289	Removed in mature form.
FT	ACT SITE	183	183	By similarity.
SEQ	SEQUENCE	289 AA:	31704 MW; 883D3E3242807B26 CR664;	
Query Match			96.7%; Score 1384; DB 1; Length 289;	
Best Local Similarity			96.2%; Pred. No. 2.8e-100;	
Matches		278;	Conservative 5; Mismatches 6; Indels 0; Gaps 0	
QY		1	MIRPLVLSLLILITLPLTPPAVEGDVSFRLSGATSSSYGFISLNKALPNEKRLYIPIL	60
DB		1	MIRPLVLSLLILITLPLTPPAVEGDVSFRLSGATSSSYGFISLNKALPNEKRLYIPIL	60
QY		61	RSLSPGSORVALIHLTNYADETISVAIDVTNYINGYAGDTSYFPNEASATFEAAKCYVK	120
DB		61	RSLSPGSORVALIHLTNYADETISVAIDVTNYINGYAGDTSYFPNEASATFEAAKCYVK	120
QY		121	DAMRKVTLPYSGNVERLQTAAKIRENIPLGIPALDSAITLLFFYNANSAAALMWLIOS	180
DB		121	DAKRKVTLPYSGNVERLQIAAGKIRENIPLGIPALDSAITLLFFYNANSAAALMWLIOS	180
QY		181	TSEARVYFIEQOIGKRVDTFLPSLAITISLNSWSALSQIOIASTNNGQFESPVLIN	240
DB		181	TSEARVYFIEQOIGKRVDTFLPSLAITISLNSWSALSQIOIASTNNGQFETPVLIN	240
QY		241	AONQRVITITNADGVTSINIALLNRRNMAAMDVDVPTQSGGCSYAL	289
DB		241	AONQRVITITNADGVTSINIALLNRRNMAAIDDDVPAQSGGCSYAL	289

RESULT	6
ID	Q41611
AC	Q41611
DT	01-NOV-1996 (TrEMBLrel. 01, Created)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Trichosanthin (Fragment).
OS	Trichosanthes kirilowii (Mongolian snake-gourd).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC	eumustelids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX	NCBI_TaxID=3677;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Bao Y., Chu R., Han J., Zhang H., Pan N., Gu X., Chen Z.;
RT	"Cloning and sequencing of trichosanthin gene and its expression in
RT	Escherichia coli and tobacco plant."
RL	Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 36:669-676 (0).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Xu L.;
RL	Submitted (APR-1995) to the EMBL/Genbank/DBJ databases.
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC	-1- specific adenosine on the 28S rRNA.
CC	-1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR	EMBL; U25675; AAA70036.1; -.
DR	HSSP; P09989; 1MRJ.
DR	GO; GO:0016787; F:hydrolase activity; IEA.
DR	GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR	GO; GO:0006952; P:defense response; IEA.
DR	GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR	GO; GO:0009405; P:papainogenesis; IEA.
DR	InterPro; IPR001574; RIP.
DR	Pfam; PF00161; RIP; 1.
DR	PRINTS; PR00396; SHIGARICIN.
DR	PROSITE; PS00275; SHIGA_RICIN; 1.
KW	Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
RT	270
SEQUENCE	270 AA; 29993 MW; 3D73FB461EABE8D4 CEC64;

Query Match 88.7%; Score 1269; DB 2; Length 270;  
 Best Local Similarity 95.2%; Pred. No. 2.6e-91;  
 Matches 257; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MIRFLVSLILITLFLTPPAVEGDVSRISGATSSSYGVFISNLKALPNERKLYDIPIL 60  
 DB 1 MIRFLVSLILITLFLTPPAVEGDVSRISGATSSSYGVFISNLKALPNERKLYDIPIL 60

QY 61 RSSLPSSQRYALHLTNVADETSVAIDVTNNYIMGRAGDTSYFENEASATEAAKYVK 120  
 DB 61 RSSLPSSQRYALHLTNVADETSVAIDVTNNYIMGRAGDTSYFENEASATEAAKYVK 120

QY 121 DAMRKVTLPYSGNVERLOTAAGKIRENIPGLPALDSAITTLFPYNNASAALMVLIO 180  
 DB 121 DAMRKVTLPYSGNVERLOTAAGKIRENIPGLPALDSAITTLFPYNNASAALMVLIO 180

QY 181 TSEAAKYKFEQOIGKRVDTPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240  
 DB 181 TSEAAKYKFEQOIGKRVDTPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240

QY 241 AONQRTITNVDAVGTSTNIALLNRMMA 270  
 DB 241 AONQRTITNVDAVGTSTNIALLNRMMA 270

RESULT 7  
 ID 06PRG5 PRELIMINARY; PRT; 270 AA.  
 AC 06PRG5;  
 DT 05-JUL-2004 (TEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
 DE Trichomastelin (Fragment).  
 OS Name=tcsm;  
 GN Trichosanthes kirilowii (Mongolian snake-gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.  
 OC NCBI\_TaxID=3677;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA M.S., An C., Chen J., Wang Y., Yuan H., Chen Z.;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 specific adenosine on the 28S rRNA.  
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
 DR EMBL: AY584242; AAS92579.1; -.  
 DR HSSP: P16094; 1AHC.  
 DR GO: GO:0016787; F:hydrolase activity; IEA.  
 DR GO: GO:0030598; F:RNA N-glycosylase activity; IEA.  
 DR GO: GO:0006952; P:defense response; IEA.  
 DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
 DR GO: GO:0009405; P:pathogenesis; IEA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP.  
 DR PRINTS: PRO0396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.  
 FT NON TER 270  
 SQ SEQUENCE 270 AA; 29649 MW; 5BB513B754F9B769 CRC64;

Query Match 88.3%; Score 1264; DB 2; Length 270;  
 Best Local Similarity 95.6%; Pred. No. 6.4e-91;  
 Matches 258; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MIRFLVSLILITLFLTPPAVEGDVSRISGATSSSYGVFISNLKALPNERKLYDIPIL 60  
 DB 1 MIRFLVSLILITLFLTPPAVEGDVSRISGATSSSYGVFISNLKALPNERKLYDIPIL 60

QY 61 RSSLPSSQRYALHLTNVADETSVAIDVTNNYIMGRAGDTSYFENEASATEAAKYVK 120  
 DB 61 RSSLPSSQRYALHLTNVADETSVAIDVTNNYIMGRAGDTSYFENEASATEAAKYVK 120

QY 121 DAMRKVTLPYSGNVERLOTAAGKIRENIPGLPALDSAITTLFPYNNASAALMVLIO 180  
 DB 121 DAMRKVTLPYSGNVERLOTAAGKIRENIPGLPALDSAITTLFPYNNASAALMVLIO 180

QY 181 TSEAAKYKFEQOIGKRVDTPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240  
 DB 181 TSEAAKYKFEQOIGKRVDTPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240

QY 241 AONQRTITNVDAVGTSTNIALLNRMMA 270  
 DB 241 AONQRTITNVDAVGTSTNIALLNRMMA 270

QY 121 DAMRKVTLPYSGNVERLOTAAGKIRENIPGLPALDSAITTLFPYNNASAALMVLIO 180  
 DB 121 DAMRKVTLPYSGNVERLOTAAGKIRENIPGLPALDSAITTLFPYNNASAALMVLIO 180

QY 181 TSEAAKYKFEQOIGKRVDTPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240  
 DB 181 TSEAAKYKFEQOIGKRVDTPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240

QY 241 AONQRTITNVDAVGTSTNIALLNRMMA 270  
 DB 241 AONQRTITNVDAVGTSTNIALLNRMMA 270

RESULT 8  
 ID 08LPV7 PRELIMINARY; PRT; 270 AA.  
 AC 08LPV7;  
 DT 01-OCT-2002 (TEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
 DE Trichosanthin precursor (Fragment).  
 OS Name=trcs;  
 GN Trichosanthes kirilowii (Mongolian snake-gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.  
 OC NCBI\_TaxID=3677;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yuan H., Wang Y., Liu T., An C., Chen Z.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 specific adenosine on the 28S rRNA.  
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
 DR EMBL: AY082348; AAM22782.1; -.  
 DR PIR: JCS032; JCS032.  
 DR HSSP: P09989; 1MRJ.  
 DR GO: GO:0016787; F:hydrolase activity; IEA.  
 DR GO: GO:0030598; F:RNA N-glycosylase activity; IEA.  
 DR GO: GO:0006952; P:defense response; IEA.  
 DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
 DR GO: GO:0009405; P:pathogenesis; IEA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PRO0396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.  
 FT CHAIN 1 23  
 FT NON TER 270  
 FT SIGNAL 24 >270  
 FT trichosanthin.  
 SQ SEQUENCE 270 AA; 29683 MW; 531713B754F9B769 CRC64;

Query Match 88.1%; Score 1260; DB 2; Length 270;  
 Best Local Similarity 95.2%; Pred. No. 1.3e-90;  
 Matches 257; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 MIRFLVSLILITLFLTPPAVEGDVSRISGATSSSYGVFISNLKALPNERKLYDIPIL 60  
 DB 1 MIRFLVSLILITLFLTPPAVEGDVSRISGATSSSYGVFISNLKALPNERKLYDIPIL 60

QY 61 RSSLPSSQRYALHLTNVADETSVAIDVTNNYIMGRAGDTSYFENEASATEAAKYVK 120  
 DB 61 RSSLPSSQRYALHLTNVADETSVAIDVTNNYIMGRAGDTSYFENEASATEAAKYVK 120

QY 121 DAMRKVTLPYSGNVERLOTAAGKIRENIPGLPALDSAITTLFPYNNASAALMVLIO 180  
 DB 121 DAMRKVTLPYSGNVERLOTAAGKIRENIPGLPALDSAITTLFPYNNASAALMVLIO 180

QY 181 TSEAAKYKFEQOIGKRVDTPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240  
 DB 181 TSEAAKYKFEQOIGKRVDTPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240

QY 241 AONQRTITNVDAVGTSTNIALLNRMMA 270  
 DB 241 AONQRTITNVDAVGTSTNIALLNRMMA 270

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DB      241 AONQRTIANVAVGVTSTNIAFLNNMMA 270
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RESULT 9
ID      Q6BB04      PRELIMINARY;      PRT;      247 AA.
AC      Q6BB04;
DT      25-OCT-2004 (TrEMBLrel. 28, Created)
DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE      Trichosanthin (Fragment).
GN      Name=TCS;
OS      Trichosanthes kirilowii (Mongolian snake-gourd).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosida I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX      NCBI_TaxID=3677;

SEQUENCE FROM N.A.
RP      M1 S.-L., Wang Y., Li Y.-Y., Chen Z.-L., An C.-C.;
RA      "Trichosanthes kirilowii trichosanthin (TCS) mature peptide gene.";
RT      Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases
RL      -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC      specific adenosine on the 28S rRNA.
CC      -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR      EMBL; AY669811; AAT91090.1; -.
DR      GO; GO:0030598; F:ribosome N-glycosylase activity; IEA.
DR      GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR      InterPro; IPR001574; RIF.
DR      Pfam; PF00161; RIF, 1.
DR      PRINTS; PR00396; SHIGARICIN.
DR      PROSITE; PS00275; SHIGA_RICIN; 1.
KW      Hydrolyase; Plant defense; Protein synthesis inhibitor; Toxin.
FT      NON_TER
FT      CHAIN
FT      NON_TER
FT      NON_TER
SQ      SEQUENCE      247 AA; 27172 MW; 6CBA762884F89CCE CRC64;

Query Match
Best Local Similarity 83.5%; Score 1195; DB 2; Length 247;
Matches 241; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADDTI 83
DB      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADDTI 60
QY      84 SVAIDVTNYYIMGYRAGDTSYFENESATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 143
DB      61 SVAIDVTNYYIMGYRAGDTSYFENESATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120
QY      144 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSEARARYFIEQIGKRVDKTEL 203
DB      121 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSEARARYFIEQIGKRVDKTEL 180
QY      204 PSIAIISLNSWSALSQIOIASTNNGQFESPVVLINQONRVITTNVAGVTSNIALI 263
DB      181 PSIAIISLNSWSALSQIOIASTNNGQFETPPVVLINQONRAITNVDAVTSNIALI 240
QY      264 LNRNNMA 270
DB      241 LNRNNMA 247

RESULT 10
ID      Q9JRE3      PRELIMINARY;      PRT;      247 AA.
AC      Q9JRE3;
DT      01-OCT-2000 (TrEMBLrel. 15, Created)
DT      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Trichobaklin (Fragment).
GN      Name=TBK;

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OS      Trichosanthes sp. Bac Kan 8-98.
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosida I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX      NCBI_TaxID=118182;

SEQUENCE FROM N.A.
RP      MEDLINE=21476888; PubMed=11592913;
RA      Van Chi P., Quoc Truong H., Thuy Ha N., Chung W.I., Binh L.T.;
RT      "Characterization of trichobaklin, a type I ribosome-inactivating
RL      protein from Trichosanthes sp. Bac Kan 8-98.";
CC      Biochem. Appl. Biochem. 34:85-92(2001).
CC      -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC      specific adenosine on the 28S rRNA.
CC      -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR      EMBL; AB033324; BAA92530.1; -.
DR      HSSP; P09989; 1J4G.
DR      GO; GO:0016787; F:hydrolase activity; IEA.
DR      GO; GO:0030598; F:ribosome N-glycosylase activity; IEA.
DR      GO; GO:0006952; P:defense response; IEA.
DR      GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR      GO; GO:0009405; P:patogenesis; IEA.
DR      InterPro; IPR001574; RIF.
DR      Pfam; PF00161; RIF, 1.
DR      PRINTS; PR00396; SHIGARICIN.
DR      PROSITE; PS00275; SHIGA_RICIN; 1.
KW      Hydrolyase; Plant defense; Protein synthesis inhibitor; Toxin.
FT      NON_TER
FT      NON_TER
FT      NON_TER
SQ      SEQUENCE      247 AA; 27199 MW; 89811AC32892F03F CRC64;

Query Match
Best Local Similarity 82.9%; Score 1187; DB 2; Length 247;
Matches 240; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADDTI 83
DB      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADDTI 60
QY      84 SVAIDVTNYYIMGYRAGDTSYFENESATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 143
DB      61 SVAIDVTNYYIMGYRAGDTSYFENESATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120
QY      144 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSEARARYFIEQIGKRVDKTEL 203
DB      121 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSEARARYFIEQIGKRVDKTEL 180
QY      204 PSIAIISLNSWSALSQIOIASTNNGQFESPVVLINQONRVITTNVAGVTSNIALI 263
DB      181 PSIAIISLNSWSALSQIOIASTNNGQFETPPVVLINQONRAITNVDAVTSNIALI 240
QY      264 LNRNNMA 270
DB      241 LNRNNMA 247

RESULT 11
ID      R1P1_BRVDI      STANDARD;      PRT;      290 AA.
AC      P33185; Q9S819;
DT      01-OCT-1993 (Rel. 27, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      Ribosome-inactivating protein bryodin I precursor (EC 3.2.2.22) (rRNA
DE      N-glycosidase) (BDI).
OS      Bryonia dioica (Red bryony).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosida I; Cucurbitales; Cucurbitaceae; Bryonia.
OX      NCBI_TaxID=3652;

SEQUENCE FROM N.A., MUTAGENESIS OF GLU-212, AND X-RAY CRYSTALLOGRAPHY
RP      (2.1 ANGSTROMS).

```



RC TISSUE=Leaf;  
 RX MEDLINE=97228081; PubMed=9115985; DOI=10.1021/b1962474+;  
 RA Gwialk S.L., Neubauer M., Klei H.E., Chang C.Y., Einspahr H.M.,  
 RA Siegal C.B.;  
 RT "Molecular, biological, and preliminary structural analysis of  
 RT recombinant bryodin 1, a ribosome-inactivating protein from the plant  
 RT Bryonia dioica.";  
 RL Biochemistry 36:3095-3103(1997).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Siegal C.B.;  
 RT "Cloning and expression of a gene encoding bryodin 1 from Bryonia  
 RT dioica.";  
 RL Patent number US5541110, 30-JUL-1996.  
 [3]  
 RP SEQUENCE OF 24-66.  
 RC TISSUE=Seed;  
 RX MEDLINE=89326691; PubMed=2753596;  
 RA Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,  
 RA Lappi D.;  
 RT "N-terminal sequence of some ribosome-inactivating proteins.";  
 RL Int. J. Pept. Protein Res. 33:263-267(1989).  
 [4]  
 RP SEQUENCE OF 24-43.  
 RC TISSUE=Root;  
 RX MEDLINE=95151812; PubMed=7849072;  
 RA Siegal C.B., Gwialk S.L., Chace D., Wolff E.A., Mixan B.,  
 RA Marquardt H.;  
 RT "Characterization of ribosome-inactivating proteins isolated from  
 RT Bryonia dioica and their utility as carcinoma-reactive  
 RT immunocjugates.";  
 RL Bioconj. Chem. 5:423-429(1994).  
 CC -1- FUNCTION: Ribosome-inactivating protein of type 1, inhibits  
 CC protein synthesis in animal cells.  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- PTM: Appears to undergo proteolytic cleavage in the C-terminal to  
 CC produce a shorter protein.  
 CC -1- BIOTECNOLOGY: Especially useful as immunotoxin for  
 CC pharmacological applications as it has low toxicity in rats and  
 CC mice but is potent once inside target cells.  
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
 CC Type 1 RIP subfamily.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL, 124020; -1 NOT\_ANNOTATED\_CDS.  
 CC PIR, S16491; S16491.  
 DR PDB; 1BRX; X-ray; Y/Z=23-270.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KM 3D-structure: Direct protein sequencing; Glycoprotein; Hydrolase;  
 KM Multigene family; Plant defense; Protein synthesis inhibitor; Signal;  
 KM Toxin.  
 FT STGNAL 1 23  
 FT CHAIN 24 270  
 FT PROPER 271 290  
 FT ACT\_SITE 183 183  
 FT ACT\_SITE 212 212  
 FT CARBOHYD 214 214  
 FT CARBOHYD 250 250  
 FT MUTAGEN 212 212  
 FT CONFLICT 61 65  
 FT STRAND 25 28  
 FT TURN 30 31

FT HELIX 34 46  
 FT TURN 47 54  
 FT STRAND 50 54  
 FT TURN 55 56  
 FT STRAND 57 60  
 FT HELIX 66 69  
 FT STRAND 70 76  
 FT TURN 78 79  
 FT STRAND 82 88  
 FT TURN 89 92  
 FT STRAND 93 99  
 FT TURN 100 101  
 FT STRAND 102 105  
 FT HELIX 109 114  
 FT TURN 115 117  
 FT TURN 120 121  
 FT STRAND 124 127  
 FT HELIX 134 141  
 FT TURN 142 142  
 FT HELIX 145 147  
 FT STRAND 150 150  
 FT HELIX 152 163  
 FT TURN 164 165  
 FT HELIX 167 186  
 FT STRAND 187 187  
 FT HELIX 188 196  
 FT STRAND 202 202  
 FT HELIX 206 213  
 FT TURN 214 214  
 FT HELIX 215 225  
 FT TURN 226 230  
 FT STRAND 231 239  
 FT TURN 241 242  
 FT STRAND 245 250  
 FT TURN 251 252  
 FT HELIX 254 257  
 FT TURN 258 259  
 FT STRAND 260 260  
 FT STRAND 263 263  
 FT HELIX 266 268  
 SQ SEQUENCE 290 AA; 31788 MW; E966CD9C031A42DB CRC64;  
 Query Match 81.9%; Score 1171.5; DB 1; Length 290;  
 Best Local Similarity 81.4%; Pred. No. 1,2e-83;  
 Matches 226; Conservative 26; Mismatches 27; Indels 1; Gaps 1;  
 QY 1 MIFPLVSLILITLFTTPAVBGDVSPRLSGATSSSYGVFISYLKALPNERKLYDIPLL 60  
 Db 1 MIKLVLMILITLFTKSPVBEQVSPRLSGATSSYGVFISYLKALPNERKLYDIPLL 60  
 QY 61 RSSLPSSQRYVALIHLTNVADETISVADVTNYIMGYRAGDTSYFFNEASATEAKYVEK 120  
 Db 61 RSSISGSGRYTLHLTNVADETISVADVTNYIMGYRAGDVSYPNEASATEAKYVEK 120  
 QY 121 DAMRKTLTPYSGNVEQLQTPAGKIRENIPPLGALDASATTLFYNNANSAASLMLVLIQS 180  
 Db 121 DAKKVTLPYSGNVEQLQTPAGKIRENIPPLGALDASATTLFYNNANSAASLMLVLIQS 180  
 QY 181 TSEPAARYKFLQOIGKRVKTFPLSPATISLENSWGLSKQIQIASTNNGQFSPVPLIN 240  
 Db 181 TSESARYKFLQOIGKRVKTFPLSPATISLENSWGLSKQIQIASTNNGQFSPVPLIN 240  
 QY 241 AONQRTITNVDAVVTSNIALNLNNNAAMDDVPMQ-SFGCGSYAL 289  
 Db 241 GNNQVRSITNASARVVTSNIALNLNNNAAMDDVPMQ-SFGCGSYAL 290  
 RESULT 12  
 RIPL\_MOMCH STANDARD; PRT; 286 AA.  
 ID RIPL\_MOMCH  
 AC P16094; P24697;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 25-OCT-2004 (rel. 45, Last annotation update)

DE Ribosome-inactivating protein momordin I precursor (EC 3.2.2.22) (rRNA

DE N-glycosidase) (Alpha-momorcharin) (Alpha-MMC).

OS Momordica charantia (Bitter melon) (Balsam pear).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eucotiled I; Cucurbitales; Cucurbitaceae; Momordica.

NCBI\_TaxID=3673;

[1]

RP SEQUENCE FROM N.A.

RC TISSUE=Seed;

RX MEDLINE=91159486; PubMed=2001404; DOI=10.1016/0167-4781(91)90070-3;

RA Ho W.K.R., Liu S.C., Shaw P.C., Yeung H.W., Ng T.B., Chan W.Y.;

RT "Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating

RT protein.";

RL Biochim. Biophys. Acta 1088:311-314(1991).

RN [2]

RP SEQUENCE OF 24-38.

RC TISSUE=Seed;

RX MEDLINE=89326691; PubMed=2753596;

RA Montecucchi P.C., Lazzarini A.M., Barbieri L., Stipe F., Soria M.,

RA Lapi D.;

RT "N-terminal sequence of some ribosome-inactivating proteins.";

RL Int. J. Pept. Protein Res. 33:263-267(1989).

RN [3]

RP SEQUENCE OF 24-70.

RC TISSUE=Seed;

RX MEDLINE=89005108; PubMed=3262509;

RA Casellas P., Dussosoy D., Palasca A.I., Barbieri L., Guillemot J.C.,

RA Ferrara P., Bolognesi A., Genin P., Stipe F.;

RT "Trichostatin, a ribosome-inactivating protein from the seeds of

RT Trichosanthes kirilowii Maximowicz. Purification, partial

RT characterization and use for preparation of immunotoxins.";

RL Eur. J. Biochem. 176:581-586(1988).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

RX MEDLINE=94356447; PubMed=8075985;

RA Ren J., Wang Y., Dong Y., Stuart D.I.;

RT "The N-glycosidase mechanism of ribosome-inactivating proteins implied

RT by crystal structures of alpha-momorcharin.";

RL Structure 2:7-16(1994).

RN [5]

RP X-RAY CRYSTALLOGRAPHY (2.16 ANGSTROMS).

RX MEDLINE=94192822; PubMed=8143869; DOI=10.1016/0014-5793(94)80491-5;

RA Husain J., Tickle I.J., Wood S.P.;

RT "Crystal structure of momordin, a type I ribosome inactivating protein

RT from the seeds of Momordica charantia.";

RL FEBS Lett. 342:154-158(1994).

RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=95344383; PubMed=7619070;

RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;

RT "Studies on crystal structures, active-centre geometry and

RT dehydrating mechanism of two ribosome-inactivating proteins.";

RL Biochem. J. 309:285-298(1995).

CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one

CC specific adenosine on the 28S rRNA.

CC -I- SIMILARITY: Belongs to the ribosome-inactivating protein family.

CC Type 1 RIP subfamily.

CC -----

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CC -----

CC EMBL; X57682; CAA0869.1; -

DR PIR; S14273; RLPUG.

DR PDB; 1AH4; X-ray; @=24-269.

DR PDB; 1AH6; X-ray; @=24-269.

DR PDB; 1AHC; X-ray; @=24-269.

DR PDB; 1F8Q; X-ray; A=24-286.

DR PDB; 1MOM; X-ray; @=24-269.

DR PDB; 1MRG; X-ray; @=24-286.

DR PDB; 1MRH; X-ray; @=24-286.

DR PDB; 1MRI; X-ray; @=24-286.

DR GLYCONSULEDB; P16094; -

DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR PROSITE; PS00275; SHIGA\_RICIN; 1.

KM 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;

KW Plant defense; Protein synthesis inhibitor; Signal; Toxin.

FT SIGNAL 1 23

FT CHAIN 24 269

FT PROPEP 270 286

FT ACT\_SITE 183 183

FT CARBOHYD 250 250

FT STRAND 25 28

FT HELIX 34 47

FT STRAND 50 54

FT TURND 55 56

FT STRAND 57 60

FT HELIX 66 69

FT STRAND 70 76

FT TURND 78 79

FT STRAND 82 88

FT TURND 89 92

FT STRAND 93 99

FT TURND 100 101

FT STRAND 102 105

FT HELIX 109 114

FT TURND 115 117

FT TURND 120 121

FT STRAND 124 127

FT HELIX 134 141

FT HELIX 145 147

FT STRAND 150 150

FT HELIX 152 162

FT TURND 163 163

FT HELIX 167 186

FT STRAND 187 187

FT HELIX 188 195

FT TURND 196 197

FT STRAND 202 202

FT HELIX 206 225

FT TURND 226 230

FT STRAND 231 238

FT TURND 240 241

FT STRAND 246 250

FT TURND 251 252

FT HELIX 254 258

FT TURND 259 259

FT STRAND 260 260

FT STRAND 263 263

FT HELIX 266 268

SQ SEQUENCE 286 AA; 31532 MW; E1B013ABBC216CF CRC64;

Query Match 60.6%; Score 866.5; DB 1; Length 286;

Best Local Similarity 63.3%; Pred. No. 9.7e-60;

Matches 179; Conservative 40; Mismatches 63; Indels 1; Gaps 1;

QY 1 MRFFVLSILITLTLTPAYEGDVSPRLSGATSSGVFISNLRKALPNRKLYDPL 60

DB 1 MSRFVLSFLIATPLGSGIVGDVSPRLSGADPSYGMFKDLNNALPFEKYNITPL 60

QY 61 RSSLPQSQRVALIHLTNYADETISVAIDVTWYIMGWYRAGDTSYFENEASATEAKYVF 120

DB 61 LPSVSGAGRYLMLHFNVDKTIITVAVDVTWYIMGWYRAGDTSYFENEASATEAKYVF 120

QY 121 DAMRVTLLPYSGNYERLQTAAGKIRENIPGLIPALDSAITTLFPYNNANSASALMVLQ 180

DB 121 DARRKITLPYSGNYERLQIAAGKPREKIPIGHPALDSAITTLHYDSTAAAGALVLIQT 180

OY 181 TSEARAKYFIEQOIGKRVDTFLPSLATISLENSMSALSKOIQIATNNQFESSPVLLIN 240  
 DB 181 TSEARAKYFIEQOIGKRVDTFLPSLATISLENSMSALSKOIQIATNNQFESSPVLLIN 240  
 OY 241 AONORVITTVNDAVGTSTNIALILNRNMAAMD-DVPMTOSE 282  
 DB 241 AONORVITTVNDAVGTSTNIALILNRNMAAMD-DVPMTOSE 282  
 DB 241 NKGRRVQITNTVTSKVTSNIGLLNTNTNINAGNDGVDSTTHGF 283

## RESULT 13

RIPA LUFCY STANDARD; PRT; 277 AA.

AC 000465;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 29-MAR-2004 (Rel. 43, Last annotation update)  
 DE Ribosome-inactivating protein luffin-alpha precursor (EC 3.2.2.22)  
 DE (RNA N-glycosidase).  
 OS Luffa cylindrica (Sponge loofah) (Sponge gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Luffa.  
 OX NCBI\_TaxID=3670;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=92288316; PubMed=1600156;  
 RA Kataoka J., Habuka N., Miyano M., Masuta C., Koizumi A.;  
 RT "Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-  
 inactivating protein from luffa cylindrica."  
 RL Plant Mol. Biol. 18:1199-1202(1992).  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 specific adenosine on the 28S rRNA.  
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
 CC Type 1 RIP subfamily.

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 or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk).

CC EMBL; X62371; CAA44229.1; -  
 DR PIR; S22494; S22494.  
 DR HSSP; P16094; IAHG.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP.1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGARICIN.1.  
 KM Antiviral; Hydrolase; Plant defense; Protein synthesis inhibitor;  
 KM Signal; Toxin.  
 FT SIGNAL 1 19  
 FT CHAIN 20 277 Ribosome-inactivating protein luffin-  
 alpha.  
 FT ACT\_SITE 179 179 By similarity.  
 SQ SEQUENCE 277 AA; 30212 MW; EA17FC27998C25AC CRC64;

Query Match 56.6%; Score 809.5; DB 1; Length 277;  
 Best Local Similarity 60.6%; Pred. No. 2.7e-55;  
 Matches 168; Conservative 45; Mismatches 59; Indels 5; Gaps 3;

OY 1 MIRFLVSLILITLFLTPPAVEGVDFRISGATSSGYVFISNLRKALPNERKLYDIP 60  
 DB 1 MKRFTV---LTLAFVFASTVADVRSLSGSSSTSKFIDGRKALPNSGTYNNITLL 57  
 OY 61 RSSLPSCORVAILHTNVADETVSVAIDVTNVIYMGIRAGDTSYFNEASATEAKYVF 120  
 DB 58 LSSASGASRYTLMQSLNDADKAITVAIDVTNVIYMGIRAGDTSYFNEASATEAKYVF 117  
 OY 121 DAMKRVTLPSYSGNVERLQTAAGKIRENIPGLPALDSAITTLFFYNNASASALMWLIQ 180

DB 118 GS-TITVLPYSGNVERLQTAAGKIRENIPGLPALDSAITTLFFYNNASASALMWLIQ 176  
 OY 181 TSEARAKYFIEQOIGKRVDTFLPSLATISLENSMSALSKOIQIATNNQFESSPVLLIN 240  
 DB 177 TSEARAKYFIEQOIGKRVDTFLPSLATISLENSMSALSKOIQIATNNQFESSPVLLIN 236  
 OY 241 AONORVITTVNDAVGTSTNIALILNRNMAAMD-DVPMTOSE 276  
 DB 237 DKGRVEITNTVTSKVTSNIGLLNTNTNINAGNDGVDSTTHGF 273

## RESULT 14

ID 000980 PRELIMINARY; PRT; 278 AA.

AC 000980;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE B-luffin.  
 OS Luffa cylindrica (Smooth loofah) (Sponge gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Luffa.  
 OX NCBI\_TaxID=3670;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=92288316; PubMed=1600156;  
 RA Kataoka J., Habuka N., Miyano M., Masuta C., Koizumi A.;  
 RT "Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-  
 inactivating protein from luffa cylindrica."  
 RL Plant Mol. Biol. 18:1199-1202(1992).  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 specific adenosine on the 28S rRNA.  
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.

CC EMBL; X62372; CAA44230.1; -  
 DR PIR; S23519; S23519.  
 DR HSSP; P22851; INIO.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
 DR GO; GO:0009405; P:patogenesis; IEA.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP.1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGARICIN.1.  
 KM Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.  
 SQ SEQUENCE 278 AA; 30586 MW; 40C26576EB53F850 CRC64;

Query Match 54.6%; Score 782; DB 2; Length 278;  
 Best Local Similarity 59.0%; Pred. No. 3.9e-53;  
 Matches 164; Conservative 47; Mismatches 63; Indels 4; Gaps 3;

OY 1 MIRFLVSLILITLFLTPPAVEGVDFRISGATSSGYVFISNLRKALPNERKLYDIP 59  
 DB 1 MKRFTVSLIITLITLFAFT--VEGANVSFSLSGADSKSYFIRALKALPNSKRVSNIP 58  
 OY 60 LRSPLPSORVAILHTNVADETVSVAIDVTNVIYMGIRAGDTSYFNEASATEAKYVF 119  
 DB 59 LPSASGASRYTLMQSLNDADKAITVAIDVTNVIYMGIRAGDTSYFNEASATEAKYVF 118  
 OY 120 KDMKRVTLPSYSGNVERLQTAAGKIRENIPGLPALDSAITTLFFYNNASASALMWLIQ 179  
 DB 119 KGS-TITVLPYSGNVERLQTAAGKIRENIPGLPALDSAITTLFFYNNASASALMWLIQ 177

QY 180 STSEAAKYFIEOQIGKRVDTFLPSLAITSLENSWALSQIOIASTNNQGESFVTLI 239  
DB 178 TTAEARFKYIEQOIGKRVDTFLPSLAITSLENSWALSQIOIASTNNQGESFVTLI 237  
QY 240 MAGNORVTTNVDAAGVTSIALTLNRRNMAADDVDP 277  
DB 238 DNKGORVEIKDVNSKVATNNIKLLNKNQIAAFDDGIP 275

RESULT 15  
RIP3\_MOMCH STANDARD; PRT; 286 AA.  
ID RIP3\_MOMCH STANDARD; PRT; 286 AA.  
AC P24817; Q41257; Q9FSH2; Q9FUV7;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ribosome-inactivating protein beta-momorcharin precursor (EC 3.2.2.22)  
DE (tRNA N-glycosidase) (MAP 30) (B-MMC).  
GN Name=MAP30; Synonyms=RIP;  
OS Momordica charantia (Bitter melon) (Balsam pear).  
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosid I; Cucurbitales; Cucurbitaceae; Momordica.  
OC NCBI\_TaxID=673;  
OX NCBI\_TaxID=673;  
RN [1]  
RP SEQUENCE FROM N.A., AND FUNCTION.  
RC TISSUE=Leaf;  
RX MEDLINE=95394347; PubMed=7665070; DOI=10.1016/0378-1119(95)00186-A;  
RA Lee-Huang S., Huang P.L., Chen H.-C., Huang P.L., Bourinbalar A.,  
RT Huang H.I., Kung H.-F.;  
RT "Anti-HIV and anti-tumor activities of recombinant MAP30 from bitter  
RT melon.";  
RL Gene 161:151-156(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Quanhong Y., Rihe P., Aisheng X.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 23-286 FROM N.A.  
RA Wei Y.-F., Cai L.-B., Zhuang W.;  
RT "Cloning rip gene and identification of its resistance to Aspergillus  
RT flauvs.";  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 23-286 FROM N.A.  
RA Nguyen Huy H., Nghiem Ngoc M., Dao Huy P., Le Tran B., Nong Van H.;  
RT "Expression of a RIP gene from Momordica charantia in E. coli.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 24-67.  
RC TISSUE=Seed;  
RX MEDLINE=91032105; PubMed=1699801; DOI=10.1016/0014-5793(90)80438-O;  
RA Lee-Huang S., Huang P.L., Nara P.L., Chen H.-C., Kung H.-F., Huang P.,  
RT "WAP 30: a new inhibitor of HIV-1 infection and replication.";  
RL FEBS Lett. 272:12-18(1990).  
RN [6]  
RP STRUCTURE BY NMR OF 24-286, AND DNA BINDING.  
RX PubMed=10571185; DOI=10.1016/S0092-8674(00)81529-9;  
RA Wang Y.-X., Neemaet N., Jacob J., Palmer I., Stahl S.J., Kaufman J.D.,  
RT Huang P.L., Huang P.L., Winslow H.E., Pommer Y., Wingfield P.T.,  
RT "Solution structure of anti-HIV-1 and anti-tumor protein MAP30:  
RT structural insights into its multiple functions.";  
RL Cell 99:433-442(1999).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 24-272.  
RX PubMed=10329776; DOI=10.1107/S0907444999003297;  
RA Yuan Y.-R., He Y.-N., Xiong J.-P., Xia Z.-X.;  
RT "Three-dimensional structure of beta-momorcharin at 2.55 A  
RT resolution.";  
RL Acta Crystallogr. D 55:1144-1151(1999).  
CC -I- FUNCTION: Possesses anti-HIV and anti-tumor activities. Inh:bits

CC HIV-1 integrase, irreversibly relax supercoiled DNA and catalyzes  
CC double-stranded breakage. Acts also as a ribosome inactivating  
CC protein.  
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
CC specific adenosine on the 28S rRNA.  
CC -I- PTM: Bound to a branched hexaaccharide.  
CC -I- MISCELLANEOUS: Manganese or zinc required for enhancing substrate  
CC binding rather than catalysis.  
CC -I- MISCELLANEOUS: The oligosaccharide does not influence the fold of  
CC the polypeptide chain and probably does not play a role in the  
CC enzymatic function.  
CC -I- MISCELLANEOUS: Is not toxic to uninfected normal cells as it  
CC cannot enter into them.  
CC -I- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
CC Type 1 RIP subfamily.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
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CC EMBL; AF284811; AAG33028.1; -;  
CC EMBL; AY523412; AAS17014.1; -;  
CC EMBL; AJ294541; CAC08217.1; -;  
CC PIR; B61318; B61318.  
CC PIR; JC4235; JC4235.  
CC PDB; 1CF5; X-ray; A/B=-.  
CC DR InterPro; IPR001574; RIP.  
CC DR Pfam; PRO0161; RIP; 1.  
CC DR PRINTS; PRO0336; SHICARICIN.  
CC DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
CC KW 3D-structure; Antiviral; Direct protein sequencing; Glycoprotein;  
CC Hydrolyase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.  
CC FT SIGNAL 1 23  
CC FT CHAIN 24 286  
CC FT ACT\_SITE 93 93  
CC FT ACT\_SITE 132 132  
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CC FT ACT\_SITE 184 184  
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Best Local Similarity 59.6%; Pred. No. 1e-51;  
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Wed Apr 13 09:27:10 2005

Qy 241 AQNORVTITNDAGVTSNIALLN 265  
Db 239 PTGERFOVTINVDSDVVKGNIKLLN 263

Search completed: April 12, 2005, 15:13:58  
Job time : 127.09 secs

us-09-905-247a-1.rup

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 12, 2005, 15:05:22 ; Search time 37.2034 Seconds  
(without alignments)  
579.883 Million cell updates/sec

Title: US-09-905-247A-1

Perfect score: 1431  
Sequence: 1 MRRFLVSLILTLFLITPA.....AAMDVVPMQSRGCSYAL 289

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/iaa/5B COMB pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB pep:\*  
5: /cgn2\_6/prodata/1/iaa/PTUS COMB pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1420	99.2	289	1	US-08-184-237-4
3	1420	99.2	289	2	US-08-482-920-4
4	1420	99.2	289	3	US-08-484-341-4
5	1420	99.2	289	3	US-08-483-502-4
6	1420	99.2	289	4	US-09-726-651A-4
7	1328	92.8	267	1	US-08-378-761A-74
8	1328	92.8	267	1	US-08-485-286-74
9	1209	84.5	247	1	US-08-488-113B-6
10	1209	84.5	247	1	US-08-477-84B-6
11	1209	84.5	247	2	US-08-646-360-6
12	1209	84.5	247	3	US-08-839-765-6
13	1209	84.5	247	3	US-09-136-389-6
14	1209	84.5	247	3	US-09-610-838-6
15	1209	84.5	247	4	US-09-711-485-6
16	1171.5	81.9	230	1	US-08-245-754A-2
17	1171.5	81.9	230	2	US-08-597-731-2
18	1137	79.5	255	1	US-07-901-707-6
19	1137	79.5	255	1	US-07-988-430-6
20	1137	79.5	255	1	US-08-425-336-6
21	1137	79.5	255	5	PCT-US92-09487-6
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23	1071	74.8	248	3	US-08-902-486-7
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26	813.5	56.8	263	1	US-08-425-336-7
27	813.5	56.8	263	1	US-08-488-113B-7

28	813.5	56.8	263	1	US-08-477-484B-7	Sequence 7, Appl1
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31	813.5	56.8	263	3	US-09-136-389-7	Sequence 7, Appl1
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33	813.5	56.8	263	4	US-09-711-485-7	Sequence 7, Appl1
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36	764	53.4	250	1	US-08-485-286-78	Sequence 78, Appl1
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42	724.5	50.6	248	1	US-08-485-286-75	Sequence 75, Appl1
43	724.5	50.6	248	1	US-08-488-113B-5	Sequence 5, Appl1
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#### ALIGNMENTS

RESULT 1  
US-07-923-692C-4  
Sequence 4, Application US/07923692C  
Patent No. 5316931  
GENERAL INFORMATION:  
APPLICANT: Donson, Jon  
APPLICANT: Grantham, George L.  
APPLICANT: Turpen, Thomas H.  
APPLICANT: Turpen, Ann Myers  
APPLICANT: Garger, Stephen J.  
APPLICANT: Grill, Laurence K.  
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Limbach & Limbach  
STREET: 2001 Ferry Building  
CITY: San Francisco  
STATE: CAL  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/923,692C  
FILING DATE: 31-JUL-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 600,244  
FILING DATE: 22-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 641,617  
FILING DATE: 16-JAN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 310,881  
FILING DATE: 17-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 160,766  
FILING DATE: 26-FEB-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 160,771  
FILING DATE: 26-FEB-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 347,637  
FILING DATE: 05-MAY-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 363,138  
FILING DATE: 08-JUN-1989

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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 219,279
/ FILING DATE: 15-JUL-1988
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Halluin, Albert P.
/ REGISTRATION NUMBER: 28,957
/ REFERENCE/DOCKET NUMBER: BIOG-20121
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-433-4150
/ TELEFAX: 415-433-8716
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 289 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-07-923-692C-4

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Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2
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/ Sequence 4, Application US/08184237
/ Patent No. 5589367
/ GENERAL INFORMATION:
/ APPLICANT: Donson, Jon
/ APPLICANT: Dawson, William O.
/ APPLICANT: Grantham, George L.
/ APPLICANT: Turpen, Thomas H.
/ APPLICANT: Turpen, Ann Myers
/ APPLICANT: Gargier, Stephen J.
/ APPLICANT: Grill, Laurence K.
/ TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Limbach & Limbach
/ STREET: 2001 Ferry Building
/ CITY: San Francisco
/ STATE: CAL
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/184,237
/ FILING DATE:
/ CLASSIFICATION: 435
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 923,692
/ FILING DATE: 31-JUL-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 600,244
/ FILING DATE: 22-OCT-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 641,617
/ FILING DATE: 16-JAN-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 310,881
/ FILING DATE: 17-FEB-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 160,766
/ FILING DATE: 26-FEB-1988
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 160,771
/ FILING DATE: 26-FEB-1988
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 347,637
/ FILING DATE: 05-MAY-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 363,138
/ FILING DATE: 08-JUN-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 219,279
/ FILING DATE: 15-JUL-1988
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Halluin, Albert P.
/ REGISTRATION NUMBER: 28,957
/ REFERENCE/DOCKET NUMBER: BIOG-20121
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-433-4150
/ TELEFAX: 415-433-8716
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 289 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-184-237-4

Query Match          99.2%; Score 1420; DB 1; Length 289;
Best Local Similarity 99.0%; Pred. No. 9.3e-138;
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MIRFLVLSLILTLFTTTPAVEGDVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60
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RESULT 3
US-08-482-920-4
/ Sequence 4, Application US/08482920
/ Patent No. 5866785
/ GENERAL INFORMATION:
/ APPLICANT: Donson, Jon
```



APPLICANT: Dawson, William O.  
APPLICANT: Grantham, George L.  
APPLICANT: Turpen, Thomas H.  
APPLICANT: Turpen, Ann Myers  
APPLICANT: Garger, Stephen J.  
APPLICANT: Grill, Laurence K.  
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS.  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,920  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 184,237  
FILING DATE: 19-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 600,244  
FILING DATE: 22-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 641,617  
FILING DATE: 16-JAN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 310,881  
FILING DATE: 17-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 160,766  
FILING DATE: 26-FEB-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 160,771  
FILING DATE: 26-FEB-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 347,637  
FILING DATE: 05-MAY-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 363,138  
FILING DATE: 08-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 219,279  
FILING DATE: 15-JUL-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 8129-112  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-482-920-4  
Query Match 99.2%; Score 1420; DB 2; Length 289;  
Best Local Similarity 99.0%; Pred. No. 9.3e-138;  
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
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DB 1 MIFVLVSLILILFLTPPAVEDVSRSLGATSSSGVTSNLRKALPNERKLYDIPLL 60  
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DB 61 RSSLPQSQRVALIHLTNVADETISVAIDVTNVIIMGVAGDTSYFNEASATEAAKVFK 120  
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US-08-484-341-4  
Sequence 4, Application US/08484341  
GENERAL INFORMATION:  
APPLICANT: Donson, Jon  
Dawson, William O.  
Grantham, George L.  
Turpen, Thomas H.  
Turpen, Ann Myers  
Garger, Stephen J.  
Grill, Laurence K.  
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Limbach & Limbach  
STREET: 2001 Ferry Building  
CITY: San Francisco  
STATE: CAL  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,341  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/184,237  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 600,244  
FILING DATE: 22-OCT-1990  
APPLICATION NUMBER: US 641,617  
FILING DATE: 16-JAN-1991  
APPLICATION NUMBER: US 310,881  
FILING DATE: 17-FEB-1989  
APPLICATION NUMBER: US 160,766  
FILING DATE: 26-FEB-1988  
APPLICATION NUMBER: US 160,771  
FILING DATE: 26-FEB-1988  
APPLICATION NUMBER: US 347,637  
FILING DATE: 05-MAY-1989  
APPLICATION NUMBER: US 363,138  
FILING DATE: 08-JUN-1989  
APPLICATION NUMBER: US 219,279  
FILING DATE: 15-JUL-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: BIOG-20121 USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-433-4150  
TELEFAX: 415-433-8716  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-08-484-341-4

Query Match 99.2%; Score 1420; DB 3; Length 289;  
Best Local Similarity 99.0%; Pred. No. 9.3e-138;  
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRFVLVSLILITLFTTPPAVEGVSFRLSGATSSSYGVFISLNKRALPNERKLYDIPLL 60  
DB 1 MRFVLVSLILITLFTTPPAVEGVSFRLSGATSSSYGVFISLNKRALPNERKLYDIPLL 60  
QY 61 RSLSPGQRYALHLTNVADETISSAIDVTNVIYINGRAGDTSYFFNEASATEAAKYVK 120  
DB 61 RSLSPGQRYALHLTNVADETISSAIDVTNVIYINGRAGDTSYFFNEASATEAAKYVK 120  
QY 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSAITTLFYNNASASALMWLIQS 180  
DB 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSAITTLFYNNASASALMWLIQS 180  
QY 181 TSEAAKYFIEQIGKRVDTFLPSLAITISLENSWSLSKQIQIASTNNQGFEPVVLIN 240  
DB 181 TSEAAKYFIEQIGKRVDTFLPSLAITISLENSWSLSKQIQIASTNNQGFEPVVLIN 240  
QY 241 AQNQRVTITNVDAVVTSTNIALLLNRNNMAAMDVPMTQSFQCGSYAL 289  
DB 241 AQNQRVTITNVDAVVTSTNIALLLNRNNMAAMDVPMTQSFQCGSYAL 289

RESULT 5  
US-08-483-502-4 ; Sequence 4, Application US/08483502

GENERAL INFORMATION:  
APPLICANT: Donson, Jon  
APPLICANT: Dawson, William O.  
APPLICANT: Grantham, George L.  
APPLICANT: Turpen, Thomas H.  
APPLICANT: Turpen, Ann Myers  
APPLICANT: Garger, Stephen J.  
APPLICANT: Grill, Laurence K.  
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,502  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/739,143  
FILING DATE:  
APPLICATION NUMBER: US 600,244  
FILING DATE: 22-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 641,617  
FILING DATE: 16-JAN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 310,881  
FILING DATE: 17-FEB-1989  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 160,766  
FILING DATE: 26-FEB-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 160,771  
FILING DATE: 26-FEB-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 347,637  
FILING DATE: 05-MAY-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 363,138  
FILING DATE: 08-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 219,279  
FILING DATE: 15-JUL-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 18604-090574  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-502-4

Query Match 99.2%; Score 1420; DB 3; Length 289;  
Best Local Similarity 99.0%; Pred. No. 9.3e-138;  
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRFVLVSLILITLFTTPPAVEGVSFRLSGATSSSYGVFISLNKRALPNERKLYDIPLL 60  
DB 1 MRFVLVSLILITLFTTPPAVEGVSFRLSGATSSSYGVFISLNKRALPNERKLYDIPLL 60  
QY 61 RSLSPGQRYALHLTNVADETISSAIDVTNVIYINGRAGDTSYFFNEASATEAAKYVK 120  
DB 61 RSLSPGQRYALHLTNVADETISSAIDVTNVIYINGRAGDTSYFFNEASATEAAKYVK 120  
QY 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSAITTLFYNNASASALMWLIQS 180  
DB 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSAITTLFYNNASASALMWLIQS 180  
QY 181 TSEAAKYFIEQIGKRVDTFLPSLAITISLENSWSLSKQIQIASTNNQGFEPVVLIN 240  
DB 181 TSEAAKYFIEQIGKRVDTFLPSLAITISLENSWSLSKQIQIASTNNQGFEPVVLIN 240  
QY 241 AQNQRVTITNVDAVVTSTNIALLLNRNNMAAMDVPMTQSFQCGSYAL 289  
DB 241 AQNQRVTITNVDAVVTSTNIALLLNRNNMAAMDVPMTQSFQCGSYAL 289

RESULT 6  
US-09-726-651A-4 ; Sequence 4, Application US/09726651A

GENERAL INFORMATION:  
APPLICANT: Donson, Jon  
APPLICANT: Dawson, William O.  
APPLICANT: Grantham, George L.  
APPLICANT: Turpen, Thomas H.  
APPLICANT: Turpen, Ann M.  
APPLICANT: Garger, Stephen J.  
APPLICANT: Grill, Laurence K.  
TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS  
FILE REFERENCE: 008010023CNU01  
CURRENT APPLICATION NUMBER: US/09/726,651A  
CURRENT FILING DATE: 2002-05-02  
PRIOR APPLICATION NUMBER: 08/483,502  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/184,237

PRIOR FILING DATE: 1994-01-19  
PRIOR APPLICATION NUMBER: 07/923,692  
PRIOR FILING DATE: 1992-07-31  
PRIOR APPLICATION NUMBER: 07/600,244  
PRIOR FILING DATE: 1990-10-22  
PRIOR APPLICATION NUMBER: 07/641,617  
PRIOR FILING DATE: 1991-01-16  
PRIOR APPLICATION NUMBER: 07/737,899  
PRIOR FILING DATE: 1991-07-26  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 289  
TYPE: PRT  
ORGANISM: Chinese Cucumber alpha-trichosanthin  
US-09-726-651A-4

Query Match 99.2%; Score 1420; DB 4; Length 289;  
Best Local Similarity 99.0%; Pred. No. 9,3e-138;  
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVSLIILFLTPPAVEGVDFRISGATSSSYGVFISNLKALPNERKLYDIPLL 60  
DB 1 MIRFLVSLIILFLTPPAVEGVDFRISGATSSSYGVFISNLKALPNERKLYDIPLL 60  
QY 61 RSSLPSSQRYALHLTNVADETISVADTNVYIMGYRAGDTSYFNEASATEAKYVFK 120  
DB 61 RSSLPSSQRYALHLTNVADETISVADTNVYIMGYRAGDTSYFNEASATEAKYVFK 120  
QY 121 DARRKTYLPYSGYVERLOTAAGKIRENIPGLPALDSAITTLFFYNANASASALMWLIOS 180  
DB 121 DARRKTYLPYSGYVERLOTAAGKIRENIPGLPALDSAITTLFFYNANASASALMWLIOS 180  
QY 181 TSEARARYFIEQIIGKRVDTFPLSLAIISELSWSALSQIOIASTNNQFESPVLIN 240  
DB 181 TSEARARYFIEQIIGKRVDTFPLSLAIISELSWSALSQIOIASTNNQFESPVLIN 240  
QY 241 AONQRTITNVDAVGTSTNIALILNRNNMAAMDDVPMTOGFCGGSYAL 289  
DB 241 AONQRTITNVDAVGTSTNIALILNRNNMAAMDDVPMTOGFCGGSYAI 289

RESULT 7  
US-08-778-761A-74  
Sequence 74, Application US/08378761A  
Patent No. 5635384  
GENERAL INFORMATION:  
APPLICANT: WALSH, TERENCE A  
APPLICANT: HEY, TIMOTHY D  
APPLICANT: MORGAN, ALICE ER  
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,761A  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651

REFERENCE/DOCKET NUMBER: 38272B  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-378-761A-74

Query Match 92.8%; Score 1328; DB 1; Length 267;  
Best Local Similarity 99.6%; Pred. No. 2.4e-128;  
Matches 266; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 GDVSPRLSGATSSSYGVFISNLKALPNERKLYDIPLLRSSLPSSQRYALHLTNVADET 82  
DB 1 GDVSPRLSGATSSSYGVFISNLKALPNERKLYDIPLLRSSLPSSQRYALHLTNVADET 82  
QY 83 ISVAIDVTNVIYIMGYRAGDTSYFNEASATEAKYVFKDAMRKVTLPSGNTERTLOTAAG 142  
DB 61 ISVAIDVTNVIYIMGYRAGDTSYFNEASATEAKYVFKDAMRKVTLPSGNTERTLOTAAG 120  
QY 143 KIRENIPGLPALDSAITTLFFYNANASASALMWLIOSTSEARARYFIEQIIGKRVDTF 202  
DB 121 KIRENIPGLPALDSAITTLFFYNANASASALMWLIOSTSEARARYFIEQIIGKRVDTF 180  
QY 203 LPSLAIISELSWSALSQIOIASTNNQFESPVLINQONQRTITNVDAVGTSTNIAL 262  
DB 181 LPSLAIISELSWSALSQIOIASTNNQFESPVLINQONQRTITNVDAVGTSTNIAL 240  
QY 263 LNRNNMAAMDDVPMTOGFCGGSYAL 289  
DB 241 LNRNNMAAMDDVPMTOGFCGGSYAI 267

RESULT 8  
US-08-485-286-74  
Sequence 74, Application US/08485286  
Patent No. 5646026  
GENERAL INFORMATION:  
APPLICANT: WALSH, TERENCE A  
APPLICANT: HEY, TIMOTHY D  
APPLICANT: MORGAN, ALICE ER  
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,286  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/378761  
FILING DATE: 26-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 38272B

Wed Apr 13 09:27:08 2005

us-09-905-247a-1.ra1

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-286-74

Query Match      92.8%; Score 1328; DB 1; Length 267;
Best Local Similarity 99.6%; Pred. No. 2.4e-128;
Matches 266; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 GVSFPLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPGSQRYALIHLTNYADETI 82
DB 1 GVSFPLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPGSQRYALIHLTNYADETI 60
QY 83 ISVAIDVTNYIMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNERLQTAAG 142
DB 61 ISVAIDVTNYIMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNERLQTAAG 120
QY 143 KIRENIPGLPALDSAITTLFYNNANSAASALMWLIQSTSEARVYFIEQIGKRVDTPL 202
DB 121 KIRENIPGLPALDSAITTLFYNNANSAASALMWLIQSTSEARVYFIEQIGKRVDTPL 180
QY 203 PSLAIIISLNSWSALSKQIQIASTNNGQFESFVVLINQONQVITTNVADGVVTSINALL 262
DB 181 PSLAIIISLNSWSALSKQIQIASTNNGQFESFVVLINQONQVITTNVADGVVTSINALL 240
QY 263 LNRNMMAMDDVPMTOGSGCSVAL 289
DB 241 LNRNMMAMDDVPMTOGSGCSVAL 267

RESULT 9
US-08-488-113B-6
; Sequence 6, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-6

Query Match      84.5%; Score 1209; DB 1; Length 247;
Best Local Similarity 99.2%; Pred. No. 3.8e-116;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 DVSFPLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPGSQRYALIHLTNYADETI 83
DB 1 DVSFPLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPGSQRYALIHLTNYADETI 60
QY 84 SVAIVTVNYIMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNERLQTAAGK 143
DB 61 SVAIVTVNYIMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPYSGNERLQTAAGK 120
QY 144 IRENIPGLPALDSAITTLFYNNANSAASALMWLIQSTSEARVYFIEQIGKRVDTPL 203
DB 121 IRENIPGLPALDSAITTLFYNNANSAASALMWLIQSTSEARVYFIEQIGKRVDTPL 180
QY 204 PSLAIIISLNSWSALSKQIQIASTNNGQFESFVVLINQONQVITTNVADGVVTSINALL 263
DB 181 PSLAIIISLNSWSALSKQIQIASTNNGQFESFVVLINQONQVITTNVADGVVTSINALL 240
QY 264 LNRNMMMA 270
DB 241 LNRNMMMA 247

RESULT 10
US-08-477-484B-6
; Sequence 6, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-484B-6

Query Match 84.5%; Score 1209; DB 1; Length 247;  
Best Local Similarity 99.2%; Pred. No. 3.8e-116;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSORYALHLTNVADDTI 83  
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSORYALHLTNVADDTI 60  
QY 84 SVAIDVTNVIYINGYRAGDTSYFFNEASATEAAKYVFKDMARKYTLFYSGYVERLQTPACK 143  
DB 61 SVAIDVTNVIYINGYRAGDTSYFFNEASATEAAKYVFKDMARKYTLFYSGYVERLQTPACK 120  
QY 144 IRENIPGLG.PALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFEQOIGRVKXFL 203  
DB 121 IRENIPGLG.PALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFEQOIGRVKXFL 180  
QY 204 PSIAIISLENSWALSQKQIQAISTNNGQFESPVVLIINAQORVTITNVDAGVVTSNIAL 263  
DB 181 PSIAIISLENSWALSQKQIQAISTNNGQFESPVVLIINAQORVTITNVDAGVVTSNIAL 240  
QY 264 LNRNMA 270  
DB 241 LNRNMA 247

RESULT 11  
US-08-646-360-6  
Sequence 6, Application US/08646360  
Patent No. 5837491  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA

ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-360-6

Query Match 84.5%; Score 1209; DB 2; Length 247;  
Best Local Similarity 99.2%; Pred. No. 3.8e-116;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSORYALHLTNVADDTI 83  
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSORYALHLTNVADDTI 60  
QY 84 SVAIDVTNVIYINGYRAGDTSYFFNEASATEAAKYVFKDMARKYTLFYSGYVERLQTPACK 143  
DB 61 SVAIDVTNVIYINGYRAGDTSYFFNEASATEAAKYVFKDMARKYTLFYSGYVERLQTPACK 120  
QY 144 IRENIPGLG.PALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFEQOIGRVKXFL 203  
DB 121 IRENIPGLG.PALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFEQOIGRVKXFL 180  
QY 204 PSIAIISLENSWALSQKQIQAISTNNGQFESPVVLIINAQORVTITNVDAGVVTSNIAL 263  
DB 181 PSIAIISLENSWALSQKQIQAISTNNGQFESPVVLIINAQORVTITNVDAGVVTSNIAL 240  
QY 264 LNRNMA 270  
DB 241 LNRNMA 247

RESULT 12  
US-08-839-765-6  
Sequence 6, Application US/08839765  
Patent No. 6146631  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 08/839,765  
FILING DATE: 15-APR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-839-765-6

Query Match 84.5%; Score 1209; DB 3; Length 247;  
Best Local Similarity 99.2%; Pred. No. 3.8e-116;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGSORYALIHILTNVADETI 83  
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGSORYALIHILTNVADETI 60  
QY 84 SVAIDVTNVIYMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPYSGNYERLQTPAAG 143  
DB 61 SVAIDVTNVIYMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPYSGNYERLQTPAAG 120  
QY 144 IRENIPLGPAIDSAITTLFYNNANGASALMWLLOSTSEARVYKRIEEOIGRVDTKFL 203  
DB 121 IRENIPLGPAIDSAITTLFYNNANGASALMWLLOSTSEARVYKRIEEOIGRVDTKFL 180  
QY 204 PSIAIISLNSWSALSQKQIASTNNGQESPVLINAGORVITITNVAGVTSNIAL 263  
DB 181 PSIAIISLNSWSALSQKQIASTNNGQESPVLINAGORVITITNVAGVTSNIAL 240  
QY 264 IRRNNMA 270  
|||||

DB 241 IRRNNMA 247

RESULT 13  
US-09-136-389-6  
Sequence 6, Application US/09136389  
Patent No. 6146850  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-136-389-6

Query Match 84.5%; Score 1209; DB 3; Length 247;  
Best Local Similarity 99.2%; Pred. No. 3.8e-116;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGSORYALIHILTNVADETI 83  
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGSORYALIHILTNVADETI 60  
QY 84 SVAIDVTNVIYMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPYSGNYERLQTPAAG 143  
|||||

Db 61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYFKDMARKVTLLPYSGYERLQTPACK 120  
QY 144 IRENIPGLPALDSATITLFFYNNANSAALMWLIQSTSEAAKYKFEQOIGKRVDTFL 203  
Db 121 IRENIPGLPALDSATITLFFYNNANSAALMWLIQSTSEAAKYKFEQOIGKRVDTFL 180  
QY 204 PSIAITSLSNSWALSQKQIQIASTNNQGFESPVVLIINAQORVTITNVDAVGTSTNIAL 263  
Db 181 PSIAITSLSNSWALSQKQIQIASTNNQGFESPVVLIINAQORVTITNVDAVGTSTNIAL 240  
QY 264 LNRNNMA 270  
Db 241 LNRNNMA 247

RESULT 14  
US-09-610-838-6  
Sequence 6, Application US/09610838  
Patent No. 6376217  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/610,838  
FILING DATE: 06-JUL-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE: 18-AUG-1998  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70,84  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-610-838-6  
Query Match 84.5%; Score 1209; DB 3; Length 247;  
Best Local Similarity 99.2%; Pred. No. 3,8e-116;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 24 DVSFRLSGATSSSGYGFISNLRKALPNERKLDIPILRSRLPSOSQYALHLTNVDETI 83  
Db 1 DVSFRLSGATSSSGYGFISNLRKALPNERKLDIPILRSRLPSOSQYALHLTNVDETI 60  
QY 84 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYFKDMARKVTLLPYSGYERLQTPACK 143  
Db 61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYFKDMARKVTLLPYSGYERLQTPACK 120  
QY 144 IRENIPGLPALDSATITLFFYNNANSAALMWLIQSTSEAAKYKFEQOIGKRVDTFL 203  
Db 121 IRENIPGLPALDSATITLFFYNNANSAALMWLIQSTSEAAKYKFEQOIGKRVDTFL 180  
QY 204 PSIAITSLSNSWALSQKQIQIASTNNQGFESPVVLIINAQORVTITNVDAVGTSTNIAL 263  
Db 181 PSIAITSLSNSWALSQKQIQIASTNNQGFESPVVLIINAQORVTITNVDAVGTSTNIAL 240  
QY 264 LNRNNMA 270  
Db 241 LNRNNMA 247

RESULT 15  
US-09-711-485-6  
Sequence 6, Application US/09711485  
Patent No. 6649742  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/711,485  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/839,765  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-711-485-6

Query Match 84.5%; Score 1209; DB 4; Length 247;  
Best Local Similarity 99.2%; Pred. No. 3.8e-116;  
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	24	DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHLTNVADETI	83
DB	1	DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHLTNVADETI	60
QY	84	SVAIIDVTNYIIMGYRAGDTSYFENESATEAAKYVFKDAMRKVTLPYSGNVERIQTAAGK	143
DB	61	SVAIIDVTNYIIMGYRAGDTSYFENESATEAAKYVFKDAMRKVTLPYSGNVERIQTAAGK	120
QY	144	IRENIPLG.PALDSAITTLLFYNNANSASALMWLIQSTSEAAKYKFEQOIGKVDKTF	203
DB	121	IRENIPLG.PALDSAITTLLFYNNANSASALMWLIQSTSEAAKYKFEQOIGKVDKTF	180
QY	204	PSLAITSLENSWSALSQIQIASTNNGOFESPVLINAOQVATITNVDAGVVTSNIAL	263
DB	181	PSLAITSLENSWSALSQIQIASTNNGOFESPVLINAOQVATITNVDAGVVTSNIAL	240
QY	264	LNRRNMA 270	
DB	241	LNRRNMA 247	

Search completed: April 12, 2005, 15:16:14  
Job time : 38.2034 secs